

Lee, B.  
1016235c7  
Seq. ID 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 21:41:13 ; Search time 165 Seconds  
(without alignments)  
731.329 Million cell updates/sec

Title: US-10-623-567a-1

Perfect score: 1573

Sequence: 1 MANNDVLRLEQKGAEADQ.....FEVKGKGVCAQTMSNSGIK 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1573	100.0	312	5	Abb07442 Human p43
2	1573	100.0	312	6	Aao29575 Human Pc2
3	1573	100.0	312	8	Adh74487 Human wou
4	1573	100.0	312	8	Adp85653 Human end
5	1573	100.0	328	4	Aab63244 Human bre
6	1343	85.4	310	2	Aar72577 Mouse EMA
7	831	52.8	166	6	Abu10452 Immunolog
8	831	52.8	166	8	Ad80906 Mammalian
9	823	52.3	166	2	Aaw14561 Endotheli
10	709	45.1	147	6	Abu10250 Immunolog
11	709	45.1	147	8	Ad80904 Mammalian
12	671	42.7	294	4	Abb59210 Drosophil
13	522.5	33.2	280	7	Abm74361 DNA clone
14	522.5	33.2	289	7	Abm73655 DNA clone
15	516	32.8	108	6	Abu10451 Immunolog
16	510.5	32.5	659	5	Ad80905 Mammalian
17	510.5	32.5	659	5	Aae19811 Corn p012
18	507	32.2	95	8	Adn99968 Novel hum
19	499	31.7	797	8	Adn73157 Thale cre
20	451	28.7	536	4	Aab47611 Human ful
21	451	28.7	536	5	Aae13487 Human tyr
22	451	28.7	536	6	Abu72380 Human ful
23	450	28.6	528	7	Adf76697 Novel hum
24	450	28.6	528	8	Adn05830 Antipsori
25	450	28.6	528	8	Adq65849 Novel hum

ALIGNMENTS

RESULT 1

ABB07442  
ID ABB07442 standard; protein; 312 AA.

XX ABB07442;

DT 23-APR-2002 (first entry)

DS Human p43 polypeptide.

XX Human; p43; cytostatic; anti-tumour; anti-angiogenic; EMAP II; cytokine;  
KW Chemotaxis.

XX Homo sapiens.

Key	Location/Qualifiers
FT Domain	1..146
FT Region	/note= "N-terminal domain"
FT Region	10..21
FT Region	/note= "beta1 strand"
FT Region	28..34
FT Region	/note= "beta2 strand"
FT Region	40..46
FT Region	/note= "beta3 strand"
FT Region	53..56
FT Region	/note= "alpha 1 helix"
FT Region	59..66
FT Region	/note= "beta4 strand"
FT Region	70..72
FT Region	/note= "beta5i strand"
FT Region	75..77
FT Region	/note= "beta6i strand"
FT Region	79..85
FT Region	/note= "beta7 strand"
FT Region	90..92
FT Region	/note= "beta8 strand"
FT Region	103..106
FT Region	/note= "beta9 strand"
FT Region	119..123
FT Region	/note= "alpha 2 helix"
FT Region	124..130
FT Region	/note= "alpha 3 helix"
FT Region	132..134
FT Region	/note= "beta10 strand"
FT Region	140..142
FT Region	/note= "beta11 strand"
FT Domain	147..312
FT	/note= "C-terminal domain"

XX WO200195927-A1.  
 XX 20-DEC-2001.  
 XX 14-JUN-2000; 2000WO-KR000630.  
 XX 14-JUN-2000; 2000WO-KR000630.  
 XX (IMAG-) IMAGENE CO LTD.  
 XX Kim S, Ko Y, Kim YS, Jo YJ;  
 XX WPI; 2002-098017/13.  
 XX N-PSDB; ABA94640.  
 XX Novel anti-tumor and anti-angiogenic agent of p43 comprises N-terminal  
 XX domain and C-terminal domain containing eleven beta-strands forming a  
 XX structural core and three flanking alpha-helices.  
 XX Claim 1; Fig 1; 35pp; English.  
 XX The invention provides an anti-tumor and anti-angiogenic agent of p43  
 XX consisting of two domains, the N-terminal domain (146 amino acids) and C-  
 XX terminal domain (166 amino acids) containing 11 beta-strands forming a  
 XX structural core and 3 flanking alpha-helices. p43 is useful as an anti-  
 XX tumor and anti-angiogenic agent. p43 and its C-terminal cytokine domain  
 XX (SMAP II) induce regression of fibrosarcoma in immunocompromised mouse  
 XX while its N-terminal domain does not. p43 is a potent cytokine as  
 XX determined by the induction of tumour necrosis factor-alpha (TNF-alpha),  
 XX interleukin-6 (IL-6), IL-8 and matrix metalloproteinase-9 or by its  
 XX activity of chemotaxis. The present sequence represents the human p43  
 XX polypeptide  
 XX Sequence 312 AA;  
 Query Match 100.0%; Score 1573; DB 5; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-135;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MANNDVAVLKEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRYENAKLKEIE 60  
 DB 1 MANNDVAVLKEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRYENAKLKEIE 60  
 QY 61 ELKQELIQAEIQNGVQKQIAPPSGTPPLHANSWSENVIQSTAVTVSSGTKEQIKGGTGE 120  
 DB 61 ELKQELIQAEIQNGVQKQIAPPSGTPPLHANSWSENVIQSTAVTVSSGTKEQIKGGTGE 120  
 QY 121 KKAKEIEKKGEKKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180  
 DB 121 KKAKEIEKKGEKKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180  
 QY 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPARKMGVLVQAMVMCASSPEKIEILA 240  
 DB 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPARKMGVLVQAMVMCASSPEKIEILA 240  
 QY 241 PPNQSVPGDRITTFDAPFGEPDKELNPKKKIWEIQPDLHTNDECVTATYKGVPEVKGKV 300  
 DB 241 PPNQSVPGDRITTFDAPFGEPDKELNPKKKIWEIQPDLHTNDECVTATYKGVPEVKGKV 300  
 QY 301 CRAFTMSNSGK 312  
 DB 301 CRAFTMSNSGK 312  
 RESULT 2  
 AAO29575  
 ID AAO29575 standard; protein; 312 AA.  
 XX AAO29575;  
 AC AAO29575;  
 XX 27-AUG-2003 (first entry)  
 DT  
 XX

DE Human Pc240 protein.  
 XX Human; differentially regulated protein; prevention; therapy; vaccine;  
 KW prostate cancer; endothelial monocyte activating polypeptide II;  
 KW gene therapy; Pc240.  
 XX Homo sapiens.  
 OS  
 PN WO2003040331-A2.  
 XX 15-MAY-2003.  
 XX 07-NOV-2002; 2002WO-US035563.  
 XX 07-NOV-2001; 2001US-0331041P.  
 PR 07-NOV-2001; 2001US-0331042P.  
 PR 18-DEC-2001; 2001US-0340251P.  
 PR 07-JAN-2002; 2002US-0344791P.  
 XX (ORIG-) ORIGENE TECHNOLOGIES INC.  
 PA Sun Z, Li X, Jay G, Kovacs KF, Fan W;  
 PI WPI; 2003-449451/42.  
 DR N-PSDB; AAL60070.  
 XX New polynucleotide for diagnosing, staging, monitoring, prognosticating,  
 PT preventing or treating, or determining the predisposition to, diseases or  
 PT conditions such as prostate cancer, and for research or forensic science.  
 XX Disclosure; Page 183-184; 100pp; English.  
 XX The present invention relates to novel differentially regulated genes and  
 CC polypeptides encoded by them. Sequences of the invention are useful in  
 CC diagnosing, staging, monitoring, prognosticating, preventing, treating or  
 CC determining the predisposition to diseases or conditions such as prostate  
 CC cancer. They may be used as molecular markers, drug targets, vaccines, in  
 CC gene therapy, research, clinical medicine or forensic science. The  
 CC present sequence is a differentially regulated prostate protein  
 CC (endothelial monocyte activating polypeptide II), Pc240  
 XX Sequence 312 AA;  
 Query Match 100.0%; Score 1573; DB 6; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-135;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MANNDVAVLKEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRYENAKLKEIE 60  
 DB 1 MANNDVAVLKEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRYENAKLKEIE 60  
 QY 61 ELKQELIQAEIQNGVQKQIAPPSGTPPLHANSWSENVIQSTAVTVSSGTKEQIKGGTGE 120  
 DB 61 ELKQELIQAEIQNGVQKQIAPPSGTPPLHANSWSENVIQSTAVTVSSGTKEQIKGGTGE 120  
 QY 121 KKAKEIEKKGEKKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180  
 DB 121 KKAKEIEKKGEKKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180  
 QY 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPARKMGVLVQAMVMCASSPEKIEILA 240  
 DB 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPARKMGVLVQAMVMCASSPEKIEILA 240  
 QY 241 PPNQSVPGDRITTFDAPFGEPDKELNPKKKIWEIQPDLHTNDECVTATYKGVPEVKGKV 300  
 DB 241 PPNQSVPGDRITTFDAPFGEPDKELNPKKKIWEIQPDLHTNDECVTATYKGVPEVKGKV 300  
 QY 301 CRAFTMSNSGK 312  
 DB 301 CRAFTMSNSGK 312  
 RESULT 3

```
ADH74487
ID ADH74487 standard; protein; 312 AA.
XX
AC ADH74487;
XX
DT 15-APR-2004 (first entry)
XX
DE Human wound healing stimulating polypeptide p43, SEQ ID 1.
XX
KW Vulnery; antiulcer; dermatological; antiallergic; antiinflammatory;
KW wound healing; burn; ulcer; trauma; post-surgical; post-child birth;
KW chronic wound; dermatitis; sunburn; chemical burn; radiation burn;
KW thermal burn; pressure ulcer; plaster ulcer; decubitus ulcer; bedsores;
KW pressure sore; diabetes; poor circulation; impetigo; intertrigo;
KW folliculitis; eczema; p43.
XX
OS Homo sapiens.
XX
PN EP1384486-A1.
XX
PD 28-JAN-2004.
XX
PF 22-JUL-2003; 2003EP-00016724.
XX
PR 22-JUL-2002; 2002KR-00042858.
XX
PA (UYSE-) UNIV SEOUL NAT IND FOUND.
XX
PI Kim S;
XX
WPI; 2004-145613/15.
XX
PT Use of p43 polypeptide, for the manufacture of pharmaceutical composition
PT intended to stimulate wound healing in a subject.
XX
PS Claim 1; SEQ ID NO 1; 20pp; English.
XX
CC The invention relates to the use of one or more polypeptides (I) chosen
CC from a polypeptide having a fully defined p43 sequence of 312 amino acids
CC as given in the specification and a polypeptide having 70% or more
CC sequence homology with (SI), for the manufacture of the pharmaceutical
CC composition (II) which is intended to stimulate wound healing in a
CC subject. The polypeptide of the invention is useful for the manufacture
CC of the pharmaceutical composition (II) which is intended to stimulate
CC wound healing in a subject. The wound is chosen from burn, ulcer, trauma,
CC post-surgical, post-child birth, chronic wound and dermatitis. The burn
CC is chosen from sun burn, chemical burn, radiation burn, and thermal burn.
CC The ulcer is chosen from pressure ulcer, plaster ulcer and decubitus
CC ulcer. The chronic wound is chosen from bedsores, pressure sores,
CC diabetes-related and poor circulation-related. The dermatitis is chosen
CC from impetigo, intertrigo, folliculitis and eczema. The current sequence
CC represents the wound healing stimulating polypeptide of the invention.
XX
SQ Sequence 312 AA;
? Query Match 100.0%; Score 1573; DB 8; Length 312;
? Best Local Similarity 100.0%; Pred. No. 1.6e-135;
? Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANNDVAVLRLEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKKEIE 60
DB 1 MANNDVAVLRLEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKKEIE 60
QY 61 ELKQELIQAEIQNGVKQIAFPSTGPLHANSWMVSENVIOSTAVTTVSSSGTKEQIKGGTGD 120
DB 61 ELKQELIQAEIQNGVKQIAFPSTGPLHANSWMVSENVIOSTAVTTVSSSGTKEQIKGGTGD 120
QY 121 KKAKEIKKGEKKEKQKQSIAGSADSKPIDVSRDLRIGCIIITARKHPDADSLYVEVD 180
DB 121 KKAKEIKKGEKKEKQKQSIAGSADSKPIDVSRDLRIGCIIITARKHPDADSLYVEVD 180
QY 181 VGEIAPRTVTVSGLVNHPVLEQMQNRWVILLCNLKPAMRGVLQSOAMVMCASSPEKIEILA 240
181 VGEIAPRTVTVSGLVNHPVLEQMQNRWVILLCNLKPAMRGVLQSOAMVMCASSPEKIEILA 240
241 PPNGSVFGDRITFDAPFGEPEKELNPKKKIWEQIQPDLHTNDECVAITYKGVFFVKGKGV 300
241 PPNGSVFGDRITFDAPFGEPEKELNPKKKIWEQIQPDLHTNDECVAITYKGVFFVKGKGV 300
301 CQAQTMNSNGIK 312
301 CQAQTMNSNGIK 312
RESULT 4
ADP85653
ID ADP85653 standard; protein; 312 AA.
XX
AC ADP85653;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human endothelial monocyte-activating polypeptide-II (EMAP-II).
XX
KW EMAP-II; endothelial monocyte-activating polypeptide-II; EMAP-2; SCYE1;
KW small inducible cytokine subfamily E member 1;
KW hyperproliferative disorder; cancer; gene therapy; human.
XX
OS Homo sapiens.
XX
PN US2004110144-A1.
XX
PD 10-JUN-2004.
XX
PF 09-DEC-2002; 2002US-00316232.
XX
PR 09-DEC-2002; 2002US-00316232.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dean NM, Dobie KW;
XX
WPI; 2004-440333/41.
XX
N-FSDB; ADP85584.
XX
PT New oligonucleotide compound that inhibits expression of EMAP-II, useful
PT for preparing a composition for treating hyperproliferative disorder,
PT e.g. cancer.
XX
PS Disclosure; Page 22-23; 35pp; English.
XX
CC The present invention relates to a compounds, compositions and methods
CC for modulating the expression of endothelial monocyte-activating
CC polypeptide-II (EMAP-II). EMAP-II is also known as EMAP-2, small
CC inducible cytokine subfamily E, member 1 (SCYE1). The compound comprises
CC antisense oligonucleotides targeted to EMAP-II. The invention is useful
CC for preparing a composition for treating hyperproliferative disorder e.g.
CC cancer. It is also useful in gene therapy. The present sequence is human
CC endothelial monocyte-activating polypeptide-II (EMAP-II). This sequence
CC is used in the invention.
XX
SQ Sequence 312 AA;
? Query Match 100.0%; Score 1573; DB 8; Length 312;
? Best Local Similarity 100.0%; Pred. No. 1.6e-135;
? Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANNDVAVLRLEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKKEIE 60
DB 1 MANNDVAVLRLEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKKEIE 60
QY 61 ELKQELIQAEIQNGVKQIAFPSTGPLHANSWMVSENVIOSTAVTTVSSSGTKEQIKGGTGD 120
DB 61 ELKQELIQAEIQNGVKQIAFPSTGPLHANSWMVSENVIOSTAVTTVSSSGTKEQIKGGTGD 120
QY 121 KKAKEIKKGEKKEKQKQSIAGSADSKPIDVSRDLRIGCIIITARKHPDADSLYVEVD 180
DB 121 KKAKEIKKGEKKEKQKQSIAGSADSKPIDVSRDLRIGCIIITARKHPDADSLYVEVD 180
QY 181 VGEIAPRTVTVSGLVNHPVLEQMQNRWVILLCNLKPAMRGVLQSOAMVMCASSPEKIEILA 240
```

Db	121	KKAKEIKKGGKGGKKQQSAGSADSKPIDVSRDLRLIGCIITARKHPDADSLYYEVD	180
Qy	181	VGSIAPRTVSVGLVNHVPLEQMONRWVILLCNLPAKXMRGVLQAMVMCASSPEKIEILA	240
Db	181	VGSIAPRTVSVGLVNHVPLEQMONRWVILLCNLPAKXMRGVLQAMVMCASSPEKIEILA	240
Qy	241	PNPGSVPGDIRITFDAPFGPEPDKELNPKKKIWEQIQPDLHTNDECVAATYKGVPEVKGKG	300
Db	241	PNPGSVPGDIRITFDAPFGPEPDKELNPKKKIWEQIQPDLHTNDECVAATYKGVPEVKGKG	300
Qy	301	CRAQTWSNSGIK 312	
Db	301	CRAQTWSNSGIK 312	
RESULT 5			
AAB63244			
XX	ID	AAB63244 standard; protein; 328 AA.	
XX	AC	AAB63244;	
XX	DT	26-MAR-2001 (first entry)	
XX	DE	Human breast cancer associated antigen protein sequence SEQ ID NO:606.	
XX	KW	Human; breast cancer; gastric cancer; prostate cancer; diagnosis;	
XX	KW	cancer associated antigen; cytostatic; cancer vaccine.	
XX	OS	Homo sapiens.	
XX	FN	WO200073801-A2.	
XX	PD	07-DEC-2000.	
XX	PF	26-MAY-2000; 2000WO-US014749.	
XX	YR	28-MAY-1999; 99US-0136526P.	
XX	PR	10-SEP-1999; 99US-0153454P.	
XX	PA	(LUDW-) LUDWIG INST CANCER RES.	
XX	PI	Obata Y;	
XX	DR	WPI; 2001-025274/03.	
XX	PT	Nucleic acids encoding breast, gastric and prostate cancer associated	
XX	PT	antigen precursors, useful for diagnosing and treating a condition	
XX	PT	characterized by expression of an abnormal amount of a protein, e.g.	
XX	PT	cancer.	
XX	PS	Example 1; Page 478; 799pp; English.	
XX	CC	AAP22422 to AAP22626, AAP22627 to AAP22773 and AAP22774 to AAP23014	
XX	CC	represent nucleotide sequences encoding human breast, gastric and	
XX	CC	prostate cancer associated antigen precursors (CAAP) respectively.	
XX	CC	AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970	
XX	CC	represent human breast, gastric and prostate CAAP protein sequence	
XX	CC	respectively. CAAPs have cytostatic activity and can be used in the	
XX	CC	production of cancer vaccines. The human CAAP proteins, peptides, nucleic	
XX	CC	acids or anti-CAAP antibodies are useful for diagnosing and treating a	
XX	CC	condition characterised by expression of an abnormal amount of a protein,	
XX	CC	e.g. cancer	
XX	SQ	Sequence 328 AA;	

Qy	61	ELKQELIQAEIQNGVKQIQIAPSPGTPPLHANSWVSENVIIQSTAVTTVSSGTTKEQIKGGTGDE	120
Db	77	ELKQELIQAEIQNGVKQIQIAPSPGTPPLHANSWVSENVIIQSTAVTTVSSGTTKEQIKGGTGDE	136
Qy	121	KKAKEKEKKGEKKKKQOSTAGSADSKPIDVSRLLDLRIGCIIITARKHPDADSLVVEVD	180
Db	137	KKAKEKEKKGEKKKKQOSTAGSADSKPIDVSRLLDLRIGCIIITARKHPDADSLVVEVD	196
Qy	181	VGEIAPRTVSGLVNHYVPLEQMQNRWVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA	240
Db	197	VGEIAPRTVSGLVNHYVPLEQMQNRWVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA	256
Qy	241	PPNGSVPGDRITFDPAFGEPPDKELNPKKKIWEQIQPDLHTNDEC VATYKGVPEVKGKGV	300
Db	257	PPNGSVPGDRITFDPAFGEPPDKELNPKKKIWEQIQPDLHTNDEC VATYKGVPEVKGKGV	316
Qy	301	CRAOTMSNSGIK 312	
Db	317	CRAOTMSNSGIK 328	
RESULT 6			
Qy	AAR72577		
ID	AAR72577	standard; protein; 310 AA.	
XX	AAR72577;		
AC	AC		
XX	25-MAR-2003 (revised)		
DT	29-SEP-1995 (first entry)		
XX	XX		
DE	Mouse EMAPII.		
XX	EMAPII; endothelial monocyte activating polypeptide II; chemotaxis;		
KW	inflammation; tissue factor; tumor; cancer; therapy; methA; sarcoma.		
XX	Mus musculus.		
XX	W09509180-A1.		
XX	06-APR-1995.		
XX	29-SEP-1994; 94WO-US011085.		
PF	29-SEP-1993; 93US-00129456.		
XX	(UYCO ) UNIV COLUMBIA NEW YORK.		
XX	Stern DM, Clauss M, Kao J, Kayton M, Libutti SK;		
PI	WPI; 1995-147389/19.		
XX	N-PSDB; AAQ86718.		
DR	New endothelial monocyte activating polypeptide II - induces chemotaxis,		
DR	inflammation and tissue factor, useful for treating tumours, also related		
PT	antibodies, DNA and active fragments.		
XX	Disclosure; Fig 4; 180pp; English.		
PS	A mouse methA sarcoma cDNA library was screened with a probe based on the		
XX	N-terminal sequence of mouse EMAPII. Overlapping clones were combined to		
CC	obtain a contiguous full-length sequence (given in AAQ86718) encoding a 33		
CC	kDa protein (AAR72577). Recombinant EMAPII was expressed in E. coli.		
CC	(Updated on 25-MAR-2003 to correct PN field.)		
XX	Sequence 310 AA;		
SQ	SQ		

Query Match	100.0%	Score 1373;	DB #	Length 328;
Best Local Similarity	100.0%	Pred. No. 1.7e-135;		
Matches 312;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MANNDVILKRLQKGAERADQIIEYLKQVSLILKEKAILQATLREKKLRVFNAKLKEIE	60	
Db	17	MANNDVILKRLQKGAERADQIIEYLKQVSLILKEKAILQATLREKKLRVFNAKLKEIE	76	

Db	1	MATNDVLRLEQKGAEDQIIEYLKQQVALLKEKAILQATMRBEKKLRVENAKLKEIE	60
Qy	61	ELKQELIQAEIQNGVKQIAPFSGTPIHANSMVSENVIOSTAV-TTVSSGTKEQIKGGTGD	119
Db	61	ELKQELILAEIHNGVEQVRVLSLPLQNTCTASESVQSPVATASPATKEQIK--AGE	118
Qy	120	EKKAKEKIEKKGEKKQKQSIAGSADSKPIIDVSRDLRLRIGCIITARKHPDADSLYVEEV	179
Db	119	EKKVKEKTEKKGEKKE-KQQAASASTDSKPIDASRLDLRIGCIITAKKHPDADSLYVEEV	177
Qy	180	DVGEIAPRTVTVSGLVNHVPLEQMQNRMVILLCNLPAKMRGVLQAMVMCASSPEKIEIL	239
Db	178	DVGEAAPRTVTVSGLVNHVPLEQMQNRMVILLCNLPAKMRGVLQAMVMCASSPEKIEIL	237
Qy	240	APPNGSVPGDRITTFDAPFGEPDKELNPKKKIWEQIQDPLHTNDECVATYKGVPEVKGK	299
Db	238	APPNGSVPGDRITTFDAPFGEPDKELNPKKKIWEQIQDPLHTNAECVATYKGAPEVKGK	297
Qy	300	VCRAQTMNSGK 312	
Db	298	VCRAQTMANSK 310	
RESULT 7			
ID	ABU10452	standard; protein; 166 AA.	
XX	XX		
AC	ABU10452;		
XX	XX		
DT	DT		
XX	XX		
DE	01-AUG-2003 (first entry)		
XX	XX		
XX	Immunological enhancement agent p43 (91-256).		
KW	Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF;		
KW	tumour necrosis factor.		
XX	XX		
OS	Mammalia.		
XX	XX		
PN	US2003004309-A1.		
XX	XX		
PD	02-JAN-2003.		
XX	XX		
PF	16-AUG-2001; 2001US-00930169.		
XX	XX		
PR	05-JUN-2001; 2001KR-00031310.		
XX	XX		
PA	(KIMS/) KIM S.		
PA	(KOY/) KO Y.		
PI	Kim S, Ko Y;		
XX	XX		
DR	WPI; 2003-447359/42.		
XX	XX		
PT	New immunological enhancement agent comprising an N-terminal peptide of		
PT	p43, useful for increasing the amount of tumor necrosis factor and		
PT	interleukin-8 to improve the immune response.		
XX	XX		
PS	Claim 3; Page 5; 12pp; English.		
XX	XX		
CC	The present sequence represents an immunological enhancement agent		
CC	comprising an N-terminal peptide of p43. The peptide can act as a		
CC	cytokine to increase the amount of tumour necrosis factor (TNF) and		
CC	interleukin-8 useful for improving an immune response and used as an		
CC	immunological enhancement agent. The present sequence represents the		
CC	amino acid sequence of the immunological enhancement agent p43 (91-256)		
XX	XX		
SQ	Sequence 166 AA;		
Query Match			
Best Local Similarity 52.8%; Score 831; DB 6; Length 166;			
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	91	MVSENVIOSTAVTTVSSGTKEQIKGGTGDKEKAKEIEKKGEKKQKQSIAGSADSKPI	150
Db	1	MVSENVIOSTAVTTVSSGTKEQIKGGTGDKEKAKEIEKKGEKKQKQSIAGSADSKPI	60
Qy	151	DVSRDLRLRIGCIITARKHPDADSLYVEEVVGEIAPRTVTVSGLVNHVPLEQMQNRMVILL	210
Db	61	DVSRDLRLRIGCIITARKHPDADSLYVEEVVGEIAPRTVTVSGLVNHVPLEQMQNRMVILL	120
Query Match			
Best Local Similarity 52.8%; Score 831; DB 6; Length 166;			
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	211	CNLPAKMRGVLQAMVMCASSPEKIEILAPPNGSVPGDRITTFDAP	256
Db	121	CNLPAKMRGVLQAMVMCASSPEKIEILAPPNGSVPGDRITTFDAP	166



ID ADS80904 standard; protein; 147 AA.  
 AC ADS80904;  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 DE Mammalian p43(1-147) protein.  
 XX  
 KW Immune response; p43; apoptotic disorder; cancer; cytostatic;  
 KW immunostimulant; cytokine-agonist.  
 XX  
 OS Mammalia.  
 XX  
 PN US2004185060-A1.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PF 14-APR-2004; 2004US-00823730.  
 XX  
 PR 05-JUN-2001; 2001KR-00031310.  
 PR 16-AUG-2001; 2001US-00930169.  
 XX  
 PA (IMAG-) IMAGENE CO LTD.  
 XX  
 PI Kim S, Ko Y;  
 XX  
 DR WPI; 2004-689153/67.  
 XX  
 PT Enhancing an immune response using an immunological enhancement agent  
 PT having the N-terminal domain of the p43 protein, useful in apoptotic  
 PT disorders such as cancer.  
 XX  
 PS Disclosure; SEQ ID NO 1; 12pp; English.  
 XX  
 CC The present invention relates to a method of enhancing an immune  
 CC response. The method involves administering an immunological enhancement  
 CC agent having the N-terminal domain of p43 protein to a cell or tissue.  
 CC The invention is useful for enhancing an immune response with an  
 CC immunological enhancement agent in apoptotic disorders such as cancer.  
 CC The present sequence is the mammalian p43(1-147) protein.  
 XX  
 SQ Sequence 147 AA;  
 Query Match 45.1%; Score 709; DB 8; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 1e-56;  
 Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MANNDVLRLEQKGAADQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKEIE 60  
 Db 1 MANNDVLRLEQKGAADQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKEIE 60  
 Qy 61 ELKQELIQAEIQNGVKQIAPSGTPLHANSMVSENVIOSTAVTTVSSGKQIKGGTGD 120  
 Db 61 ELKQELIQAEIQNGVKQIAPSGTPLHANSMVSENVIOSTAVTTVSSGKQIKGGTGD 120  
 Qy 121 KKAKEIEKKEKKEKQOISAGSADS 147  
 Db 121 KKAKEIEKKEKKEKQOISAGSADS 147  
 RESULT 12  
 ABB59210  
 ID ABB59210 standard; protein; 294 AA.  
 XX  
 AC ABB59210;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 4422.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX

OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US009231.  
 XX  
 PR 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL03313.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX  
 PS Disclosure; SEQ ID NO 4422; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABU16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 294 AA;  
 Query Match 42.7%; Score 671; DB 4; Length 294;  
 Best Local Similarity 44.9%; Pred. No. 8.6e-53;  
 Matches 141; Conservative 57; Mismatches 88; Indels 28; Gaps 5;  
 Qy 6 AVLKRLQKGAADQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKEIEELKQE 65  
 Db 2 ADLQIASNNEAEALINSIEAETISGQQ----QLVERQKQELIKENAAKAEVAAALAQ 57  
 Qy 66 LIQAEIQNGVKQIAPF-----SGTPLHANSMVSENVIOSTAVTTVSSGKQIKGGTG 118  
 Db 58 LVQLELRNGKKQIPVPGARGFCTSAAPV----VMPAAGPATAPAAPA----- 102  
 Qy 119 DEKKAKEIEKKEKKEKQOISAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEE 178  
 Db 103 -PKPAKEPKKEKKEKPAAEKPA-AAPEAPVDVGRDLRVGKIVEGRHPDADSLYLEK 160  
 Qy 179 VDVGSEIAPRTVSGLVNHPLEQNMQRVILLCNLKPAPKRGVLSQAMVMCASPEKIEI 238  
 Db 161 IDCCEAAPRTVSGLVKVFPLEEMQNLVVMCNLKPAPKRGVTSAMVMCASTPEKVEV 220  
 Qy 239 LAPNGSVPGDRITFDAPGPEPKELNPKKIWEIOPLDLTNDCEVATYKGVPEVKGK 298  
 Db 221 LSPAPGAPVPGDLVHCEGYPRQPDQALNPKPKKIFESCAPDLKTNGLVACYGAALHVPKG 280  
 Qy 299 GVCRAQTMNSNGIK 312  
 Db 281 GNVVAQILKKNVVK 294  
 RESULT 13  
 ABB74361  
 ID ABB74361 standard; protein; 280 AA.  
 XX  
 AC ABB74361;  
 XX  
 DT 17-OCT-2003 (first entry)

XX DNA clone originating in barley containing SNP sequence #771.  
XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.  
XX Hordeum vulgare.  
XX WO2003057877-A1:  
XX 17-JUL-2003.  
XX 16-DEC-2002; 2002WO-IB005403.  
XX 20-DEC-2001; 2001JP-00387059.  
XX 20-DEC-2001; 2001JP-00387131.  
XX 20-DEC-2001; 2001JP-00403299.  
XX 20-DEC-2001; 2001JP-00403300.  
XX 27-SEP-2002; 2002JP-00327515.  
XX (UYNI-) UNIV JAPAN OKAYAMA.  
XX Sato K, Takeda K, Kohara Y;  
XX WPI; 2003-587127/55.  
XX Single nucleotide polymorphism sites in barley varieties and DNA  
XX sequences containing them for analysis and identification of barley  
XX varieties and production of barley transformants with desired  
XX characteristics.  
XX Disclosure; SEQ ID XX; 284pp; Japanese.  
XX The present invention relates to oligonucleotide clones originating in  
XX barley (Hordeum vulgare) which contain single nucleotide polymorphisms  
XX (SNP). The oligonucleotides may be used for analysis of SNPs among barley  
XX varieties, identification of particular varieties and genotype-phenotype  
XX analysis, isolation of specific genes and creation of new varieties by  
XX transformation of barley varieties with them and production of new barley  
XX varieties with desired properties. The present sequence represents an  
XX oligonucleotide clone sequence featured in the specification. The  
XX sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published-pct-sequences  
XX Sequence 280 AA;  
Query Match 33.2%; Score 522.5; DB 7; Length 280;  
Best Local Similarity 45.4%; Pred. No. 3.4e-39;  
Matches 108; Conservative 42; Mismatches 77; Indels 11; Gaps 5;  
Qy 83 GTPHANSMVSENVIOSTAVTTVSSGTKEQIKG-GTGDEKKAKEKIEKKGEK-----KEK 136  
Db 46 GKPVPFLFKELQDQVEAFRIKFAQSQAERILKGOADAEAKKVAEKL--KGTKLSEGSKK 103  
Qy 137 KQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEDVGEIAPRTVVSGLVNH 196  
Db 104 KQSGSKSKTSEDSVAKLDIRVGLIRKAEKHPDADSLYVEEDVGEIAPRTVVSGLVKP 163  
Qy 197 VPLEQMQNRVILLNLCKLPKAMRGVLQAMVMCASSPE--KIEILAPNGSVPGDRITFD 254  
Db 164 IPLEEMQNRKVCVLCNLKPKVAMRGIKSHAMVLAASNEHDHTKVELVEPPESAAGVETFA 223  
Qy 255 AFPGEPDKELNPKKIKWEIQOPDLHTNDECVATYKGVPPFVKGVKVCRAOTMNSGIK 312  
Db 224 GFSGEPEASLNKSKTWEKLSADLHNSGELVACYKDVFPFTTSA-GVCKVKTIANGAIR 280  
RESULT 14  
ABM73655  
ID ABM73655 standard; protein; 289 AA.  
XX  
AC ABM73655;  
XX

DT 17-OCT-2003 (first entry)  
XX DNA clone originating in barley containing SNP sequence #65.  
XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.  
XX Hordeum vulgare.  
XX WO2003057877-A1.  
XX 17-JUL-2003.  
XX 16-DEC-2002; 2002WO-IB005403.  
XX 20-DEC-2001; 2001JP-00387059.  
XX 20-DEC-2001; 2001JP-00387131.  
XX 20-DEC-2001; 2001JP-00403299.  
XX 20-DEC-2001; 2001JP-00403300.  
XX 27-SEP-2002; 2002JP-00327515.  
XX (UYNI-) UNIV JAPAN OKAYAMA.  
XX Sato K, Takeda K, Kohara Y;  
XX WPI; 2003-587127/55.  
XX Single nucleotide polymorphism sites in barley varieties and DNA  
XX sequences containing them for analysis and identification of barley  
XX varieties and production of barley transformants with desired  
XX characteristics.  
XX Disclosure; SEQ ID XX; 284pp; Japanese.  
XX The present invention relates to oligonucleotide clones originating in  
XX barley (Hordeum vulgare) which contain single nucleotide polymorphisms  
XX (SNP). The oligonucleotides may be used for analysis of SNPs among barley  
XX varieties, identification of particular varieties and genotype-phenotype  
XX analysis, isolation of specific genes and creation of new varieties by  
XX transformation of barley varieties with them and production of new barley  
XX varieties with desired properties. The present sequence represents an  
XX oligonucleotide clone sequence featured in the specification. The  
XX sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published-pct-sequences  
XX Sequence 289 AA;  
Query Match 33.2%; Score 522.5; DB 7; Length 289;  
Best Local Similarity 45.4%; Pred. No. 3.5e-39;  
Matches 108; Conservative 42; Mismatches 77; Indels 11; Gaps 5;  
Qy 83 GTPHANSMVSENVIOSTAVTTVSSGTKEQIKG-GTGDEKKAKEKIEKKGEK-----KEK 136  
Db 55 GKPVPFLFKELQDQVEAFRIKFAQSQAERILKGOADAEAKKVAEKL--KGTKLSEGSKK 112  
Qy 137 KQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEDVGEIAPRTVVSGLVNH 196  
Db 113 KQSGSKSKTSEDSVAKLDIRVGLIRKAEKHPDADSLYVEEDVGEIAPRTVVSGLVKP 172  
Qy 197 VPLEQMQNRVILLNLCKLPKAMRGVLQAMVMCASSPE--KIEILAPNGSVPGDRITFD 254  
Db 173 IPLEEMQNRKVCVLCNLKPKVAMRGIKSHAMVLAASNEHDHTKVELVEPPESAAGVETFA 232  
Qy 255 AFPGEPDKELNPKKIKWEIQOPDLHTNDECVATYKGVPPFVKGVKVCRAOTMNSGIK 312  
Db 233 GFSGEPEASLNKSKTWEKLSADLHNSGELVACYKDVFPFTTSA-GVCKVKTIANGAIR 289  
RESULT 15  
ABU10451  
ID ABU10451 standard; protein; 108 AA.  
XX  
AC ABU10451;  
XX



```
XX 01-AUG-2003 (first entry)
DT
XX Immunological enhancement agent p43 (1-108).
DE
XX Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF;
KW tumour necrosis factor.
XX Mammalia.
OS
XX US2003004309-A1.
FN
XX 02-JAN-2003.
PD
XX 16-AUG-2001; 2001US-0030169.
PF
XX 05-JUN-2001; 2001KR-00031310.
PR
XX (KIMS/) KIM S.
PA (KOY/) KO Y.
XX
XX Kim S, Ko Y;
PI
XX WPI; 2003-447359/42.
DR
XX
XX New immunological enhancement agent comprising an N-terminal peptide of
PT p43, useful for increasing the amount of tumor necrosis factor and
PT interleukin-8 to improve the immune response.
XX
XX Claim 2; Page 5; 12pp; English.
PS
XX The present sequence represents an immunological enhancement agent
XX comprising an N-terminal peptide of p43. The peptide can act as a
XX cytokine to increase the amount of tumour necrosis factor (TNF) and
XX interleukin-8 useful for improving an immune response and used as an
XX immunological enhancement agent. The present sequence represents the
XX amino acid sequence of the immunological enhancement agent p43 (1-108)
XX
XX Sequence 108 AA;
SQ
Query Match 32.8%; Score 516; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.4e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MANNDVILKRLKQKGAEDQIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Qy 61 ELKQELIQAEIQGVKQIAFPSTPLHANSMVSENVIOSTAVTTVSSG 108
Db 61 ELKQELIQAEIQGVKQIAFPSTPLHANSMVSENVIOSTAVTTVSSG 108
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Job time : 168 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 21:47:49 ; Search time 42 Seconds  
(without alignments)  
554.536 Million cell updates/sec

Title: US-10-623-567A-1

Perfect score: 1573

Sequence: 1 MANNDVLRLEQKGAADQ.....FEVKGKGVCFRAQTMSNGIK 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pap.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pap.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1568	99.7	312	3	US-08-360-821B-36
2	1568	99.7	312	4	US-09-851-026-36
3	1568	99.7	320	4	US-09-949-016-7144
4	1510	96.0	310	1	US-08-129-456A-37
5	1343	85.4	310	1	US-08-129-456A-36
6	1343	85.4	310	2	US-08-705-868-3
7	1343	85.4	310	3	US-09-123-615-3
8	1343	85.4	310	3	US-08-360-821B-35
9	1343	85.4	310	4	US-09-851-026-35
10	931	59.2	183	3	US-08-483-534A-7
11	835	53.1	166	1	US-08-129-456A-11
12	835	53.1	166	3	US-08-360-821B-11
13	835	53.1	166	4	US-09-851-026-11
14	510.5	32.5	659	3	US-09-392-772-10
15	440.5	28.0	301	2	US-08-705-868-1
16	440.5	28.0	301	3	US-09-123-615-1
17	440.5	28.0	301	4	US-09-919-039-132
18	438.5	27.9	215	4	US-09-248-796A-19812
19	429.5	27.3	168	3	US-08-483-534A-2
20	410.5	26.1	492	4	US-09-949-016-10567
21	235	14.9	174	4	US-09-248-796A-19813
22	227	14.0	720	4	US-09-328-352-4765
23	188.5	12.0	674	4	US-09-107-532A-6201
24	186.5	11.9	648	1	US-08-451-715A-4
25	184	11.7	703	4	US-09-902-540-10686
26	182.5	11.6	111	4	US-09-489-039A-9293
27	174.5	11.1	493	4	US-09-134-000C-4034

28	157	10.0	665	3	US-08-844-059-2	Sequence 2, Appli
29	157	10.0	665	3	US-09-431-202-2	Sequence 2, Appli
30	152.5	9.7	336	4	US-09-107-433-4916	Sequence 4916, Ap
31	152.5	9.7	679	4	US-09-583-110-2751	Sequence 2751, Ap
32	147	9.3	221	4	US-09-252-991A-21654	Sequence 21654, A
33	136	8.6	716	4	US-09-489-039A-8243	Sequence 8243, Ap
34	134.5	8.6	680	4	US-09-352-991A-17566	Sequence 17566, A
35	129	8.2	690	4	US-09-540-236-3507	Sequence 3507, Ap
36	128	8.1	115	3	US-08-844-059-4	Sequence 4, Appli
37	128	8.1	115	3	US-09-431-202-4	Sequence 4, Appli
38	128	8.1	683	4	US-09-543-681A-5403	Sequence 5403, Ap
39	119.5	7.6	589	4	US-09-543-681A-7643	Sequence 7643, Ap
40	117	7.4	721	3	US-09-134-078-19	Sequence 19, Appli
41	116.5	7.4	414	5	PCT-US93-03077-3	Sequence 3, Appli
42	116.5	7.4	1093	4	US-09-949-016-11535	Sequence 11535, A
43	116.5	7.4	1093	5	PCT-US93-03077-1	Sequence 1, Appli
44	116	7.4	1118	4	US-09-949-016-6596	Sequence 6596, Ap
45	116	7.4	1120	4	US-09-949-016-10404	Sequence 10404, A

ALIGNMENTS

RESULT 1  
US-08-360-821B-36  
; Sequence 36, Application US/08360821B  
; Patent No. 6228837  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Clauss, Matthias  
; APPLICANT: Kao, Janet  
; APPLICANT: Kayton, Mark  
; APPLICANT: Libutti, Steven K  
; TITLE OF INVENTION: Endothelial Monocyte Activating  
; TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham, LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.30, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,821B  
; FILING DATE: 08-OCT-96  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 312 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-360-821B-36

Query Match 99.7%; Score 1568; DB 3; Length 312;  
Best Local Similarity 99.7%; Pred. No. 2.9e-136;  
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MANNDVLRLEQKGAADQIIIEYLKQVSLLEKAILQATLREBKLRVENAKLKKIE 60

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1 MANNDVAVLRLEQKGAADQII EYLVKQVSLLEKAILQATLREKKLRVENAKLKEIE 60
61 ELKQELIOAEIQNGVKQIAPPSTPLHANSWVSENVIOSTAVTVSSGTKEQIKGGTGDE 120
61 ELKQELIOAEIQNGVKQIAPPSTPLHANSWVSENVIOSTAVTVSSGTKEQIKGGTGDE 120
121 KKAKEKIEKKGEKKKQOSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180
121 KKAKEKIEKKGEKKKQOSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180
181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
241 PPNQSVPGDRITFDAPFGPDKELNPKKKIWEIQPDLHTNDECVATYKGVPEVKGKV 300
241 PPNQSVPGDRITFDAPFGPDKELNPKKKIWEIQPDLHTNDECVATYKGVPEVKGKV 300
301 CRAFTMSNSGIK 312
301 CRAFTMSNSGIK 312

RESULT 2
US-09-851-026-36
; Sequence 36, Application US/09851026
; Patent No. 6734168
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; Kao, Janet
; Kayton, Mark
; Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
; Polypeptide II: A Mediator Which Activates Host Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,026
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821
; FILING DATE: 08-OCT-96
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-851-026-36

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Query Match 99.7%; Score 1568; DB 4; Length 312;
Best Local Similarity 99.7%; Pred. No. 2.9e-136;
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MANNDVAVLRLEQKGAADQII EYLVKQVSLLEKAILQATLREKKLRVENAKLKEIE 60
DB 1 MANNDVAVLRLEQKGAADQII EYLVKQVSLLEKAILQATLREKKLRVENAKLKEIE 60
QY 61 ELKQELIOAEIQNGVKQIAPPSTPLHANSWVSENVIOSTAVTVSSGTKEQIKGGTGDE 120
DB 61 ELKQELIOAEIQNGVKQIAPPSTPLHANSWVSENVIOSTAVTVSSGTKEQIKGGTGDE 120
QY 121 KKAKEKIEKKGEKKKQOSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180
DB 121 KKAKEKIEKKGEKKKQOSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180
QY 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
DB 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
QY 241 PPNQSVPGDRITFDAPFGPDKELNPKKKIWEIQPDLHTNDECVATYKGVPEVKGKV 300
DB 241 PPNQSVPGDRITFDAPFGPDKELNPKKKIWEIQPDLHTNDECVATYKGVPEVKGKV 300
QY 301 CRAFTMSNSGIK 312
DB 301 CRAFTMSNSGIK 312

RESULT 3
US-09-949-016-7144
; Sequence 7144, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7144
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7144

Query Match 99.7%; Score 1568; DB 4; Length 320;
Best Local Similarity 99.7%; Pred. No. 3e-136;
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MANNDVAVLRLEQKGAADQII EYLVKQVSLLEKAILQATLREKKLRVENAKLKEIE 60
DB 9 MANNDVAVLRLEQKGAADQII EYLVKQVSLLEKAILQATLREKKLRVENAKLKEIE 68
QY 61 ELKQELIOAEIQNGVKQIAPPSTPLHANSWVSENVIOSTAVTVSSGTKEQIKGGTGDE 120
DB 69 ELKQELIOAEIQNGVKQIAPPSTPLHANSWVSENVIOSTAVTVSSGTKEQIKGGTGDE 128
QY 121 KKAKEKIEKKGEKKKQOSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180
DB 129 KKAKEKIEKKGEKKKQOSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 188
QY 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
DB 189 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 248

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Qy 241 PPNGSVPGDRITFDAPGEPDKELNPKKKIWEQIQPDLHTNDECVAITYKGVPEVKGKV 300  
 Db 249 PPNGSVPGDRITFDAPGEPDKELNPKKKIWEQIQPDLHTNDECVAITYKGVPEVKGKV 308  
 Qy 301 CQAQTSNSGIK 312  
 Db 309 CQAQTSNSGIK 320

RESULT 4  
 US-08-129-456A-37  
 ; Sequence 37, Application US/08129456A  
 ; Patent No. 5641867  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stern, David M.  
 ; APPLICANT: Clauss, Matthias  
 ; APPLICANT: Kao, Janet  
 ; APPLICANT: Kayton, Mark  
 ; APPLICANT: Libutti, Steven K.  
 ; TITLE OF INVENTION: Endothelial-Monocyte Activating  
 ; TITLE OF INVENTION: Polypeptide II: A Mediator Which  
 ; TITLE OF INVENTION: Activates Host Response  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0 Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/129,456A  
 ; FILING DATE: 29-SEP-1993  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 41735  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212 278 0400  
 ; TELEFAX: 212 391 0526  
 ; INFORMATION FOR SEQ ID NO: 37:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 310 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-129-456A-37

Query Match 96.0%; Score 1510; DB 1; Length 310;  
 Best Local Similarity 97.8%; Pred. No. 6.4e-131;  
 Matches 306; Conservative 0; Mismatches 3; Indels 4; Gaps 3;  
 Qy 1 MANNDVAVLKRLEQKGAADQIIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
 Db 1 MANNDVAVLKRLEQKGAADQIIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
 Qy 61 ELKQELIOAEIQNGVKQIAFPSTGTPHANSWMVSENVIOSTAV-TTVSSGTKEQIKGGTGD 119  
 Db 61 ELKQELIOAEIQNGVKQIAFPSTGTPHANSWMVSENVIOSTAV-TTVSSGTKEQIK--AGD 118  
 Qy 120 EKKAKEKTEKKEKKEKQKQSGTAGSDSKPIDVSRDLRIGCIITARKHPDADSLYVEEV 179  
 Db 119 EKKAKEKTEKKEKKEK--KQKQSGTAGSDSKPIDASRLDLRIGCIITARKHPDADSLYVEEV 177  
 Qy 180 DVGETAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPAMRGVLSQAMVWCASSPEKIEIL 239

Db 178 DVGEIAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPAMRGVLSQAMVWCASSPEKIEIL 237  
 Qy 240 APNGSVPGDRITFDAPGEPDKELNPKKKIWEQIQPDLHTNDECVAITYKGVPEVKGKV 299  
 Db 238 APNGSVPGDRITFDAPGEPDKELNPKKKIWEQIQPDLHTNDECVAITYKGVPEVKGKV 297  
 Qy 300 VCRAQTSNSGIK 312  
 Db 298 VCRAQTSNSGIK 310

RESULT 5  
 US-08-129-456A-36  
 ; Sequence 36, Application US/08129456A  
 ; Patent No. 5641867  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stern, David M.  
 ; APPLICANT: Clauss, Matthias  
 ; APPLICANT: Kao, Janet  
 ; APPLICANT: Kayton, Mark  
 ; APPLICANT: Libutti, Steven K.  
 ; TITLE OF INVENTION: Endothelial-Monocyte Activating  
 ; TITLE OF INVENTION: Polypeptide II: A Mediator Which  
 ; TITLE OF INVENTION: Activates Host Response  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0 Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/129,456A  
 ; FILING DATE: 29-SEP-1993  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 41735  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212 278 0400  
 ; TELEFAX: 212 391 0526  
 ; INFORMATION FOR SEQ ID NO: 36:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 310 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-129-456A-36

Query Match 85.4%; Score 1343; DB 1; Length 310;  
 Best Local Similarity 85.9%; Pred. No. 1.5e-115;  
 Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;  
 Qy 1 MANNDVAVLKRLEQKGAADQIIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
 Db 1 MATNDVAVLKRLEQKGAADQIIIEYLKQOVALLKEKAILQATMRBEKKLRVENAKLKEIE 60  
 Qy 61 ELKQELIOAEIQNGVKQIAFPSTGTPHANSWMVSENVIOSTAV-TTVSSGTKEQIKGGTGD 119  
 Db 61 ELKQELILAEIHNGVEQVRVRLSTPLQTNCTASSSVQSPSVATFASPATKEQIK--AGE 118  
 Qy 120 EKKAKEKTEKKEKKEKQKQSGTAGSDSKPIDVSRDLRIGCIITARKHPDADSLYVEEV 179  
 Db 119 EKKYKTEKTEKKEKKE--KQKQAAAATSDSKPIDASRLDLRIGCIITAKKHPDADSLYVEEV 177  
 Qy 180 DVGETAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPAMRGVLSQAMVWCASSPEKIEIL 239

Db 178 DVGEAAPTIVVSLVNHVPLEQMNRMVLLCNLKPAMRGVLSQAMVMCASSPEKVEIL 237  
Qy 240 APNGSVPGDRITFDAPGPEPKELNPKKIWEQIQPDLHTNDECVAITYKGVPEVKKG 299  
Db 238 APPNGSVPGDRITFDAPGPEPKELNPKKIWEQIQPDLHTNDECVAITYKGVPEVKKG 297  
Qy 300 VCRAQTMSNSGIK 312  
Db 298 VCRAQTMSNSGIK 310

RESULT 6

US-08-705-868-3  
; Sequence 3, Application US/08705868  
; Patent No. 5885798  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Coleman, Roger  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Murry, Lynn E.  
; TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08705,868  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0117 US  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 310 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 498910  
US-08-705-868-3

Query Match 85.4%; Score 1343; DB 2; Length 310;  
Best Local Similarity 85.9%; Pred. No. 1.5e-115;  
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

Qy 1 MANNDVAVLRLKLEQKGAADQIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
Db 1 MATNDVAVLRLKLEQKGAADQIIEYLKQVALLKEKAILQATMREKKLRVENAKLKEIE 60  
Qy 61 ELKQELIQABIQNGVKQIAPPSGTPPLHANSVMSENVIQSTAV-TTVSSSGTKEQIKGTTGD 119  
Db 61 ELKQELILAEIHNGVEQVRVRLSTPLQTNCTASESVVQSPVATTASPAKKEQIK--AGE 118  
Qy 120 EKKAKEIKKKEKKEKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYYEEV 179  
Db 119 EKKVKEKTEKKEKKE--KQSAASATDSKPIDASRLDLRIGCIITAKKHPDADSLYYEEV 177

Qy 180 DVGEIAPTIVVSLVNHVPLEQMNRMVLLCNLKPAMRGVLSQAMVMCASSPEKIEIL 239  
Db 178 DVGEAAPTIVVSLVNHVPLEQMNRMVLLCNLKPAMRGVLSQAMVMCASSPEKVEIL 237  
Qy 240 APNGSVPGDRITFDAPGPEPKELNPKKIWEQIQPDLHTNDECVAITYKGVPEVKKG 299  
Db 238 APPNGSVPGDRITFDAPGPEPKELNPKKIWEQIQPDLHTNDECVAITYKGVPEVKKG 297  
Qy 300 VCRAQTMSNSGIK 312  
Db 298 VCRAQTMSNSGIK 310

RESULT 7

US-09-123-615-3  
; Sequence 3, Application US/09123615  
; Patent No. 6090377  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Coleman, Roger  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Murry, Lynn E.  
; TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09123,615  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/705,868  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0117 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 310 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 498910  
US-09-123-615-3

Query Match 85.4%; Score 1343; DB 3; Length 310;  
Best Local Similarity 85.9%; Pred. No. 1.5e-115;  
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

Qy 1 MANNDVAVLRLKLEQKGAADQIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
Db 1 MATNDVAVLRLKLEQKGAADQIIEYLKQVALLKEKAILQATMREKKLRVENAKLKEIE 60  
Qy 61 ELKQELIQABIQNGVKQIAPPSGTPPLHANSVMSENVIQSTAV-TTVSSSGTKEQIKGTTGD 119  
Db 61 ELKQELILAEIHNGVEQVRVRLSTPLQTNCTASESVVQSPVATTASPAKKEQIK--AGE 118

Qy 120 EKKAKEKIEKKGEKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYYEEV 179  
 Db 119 EKKVKETKKEKKE-KQKSAASTDSKPIDASRLDLRIGCIITAKKHPDADSLYYEEV 177  
 Qy 180 DVGEIAPRTVVGSLVNHVPLEQONRMVILLCNLKPAKMRGVLQAMVMCASSPEKIEIL 239  
 Db 178 DVGEAAPRTVVGSLVNHVPLEQONRMVILLCNLKPAKMRGVLQAMVMCASSPEKIEIL 237  
 Qy 240 APPNGSVPGDRITFDAPFGPEPKELNPKKIKWEIQPDLHTNDECVAITYKGVPEVKKG 299  
 Db 238 APPNGSVPGDRITFDAPFGPEPKELNPKKIKWEIQPDLHTNDECVAITYKGVPEVKKG 297  
 Qy 300 VCRAQTMNSGK 312  
 Db 298 VCRAQTMNSGK 310

RESULT 8  
 US-08-360-821B-35  
 ; Sequence 35, Application US/08360821B  
 ; Patent No. 6228837  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stern, David M.  
 ; APPLICANT: Clauss, Matthias  
 ; APPLICANT: Kao, Janet  
 ; APPLICANT: Kayton, Mark  
 ; APPLICANT: Libutti, Steven K  
 ; TITLE OF INVENTION: Endothelial Monocyte Activating  
 ; TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham, LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.30, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/360,821B  
 ; FILING DATE: 08-OCT-96  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-278-0400  
 ; TELEFAX: 212-391-0525  
 ; INFORMATION FOR SEQ ID NO: 35:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 310 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-360-821B-35

Query Match 85.4%; Score 1343; DB 3; Length 310;  
 Best Local Similarity 85.9%; Pred. No. 1.5e-115;  
 Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;  
 Qy 1 MANNDVLRLEQKGAEDQIIEYLKQVSLKKEKAILQATLREBKLRVENAKLKKEIE 60  
 Db 1 MATNDVLRLEQKGAEDQIIEYLKQVSLKKEKAILQATLREBKLRVENAKLKKEIE 60  
 Qy 61 ELKQBLIQAEIQNGVKQAFPSGTPFHANSVMVSENVIQSTAV-TTVSGTKEQIKGGTGD 119  
 Db 61 ELKQBLILAEIHNGVEQVRVRLSTPLQTNCTASESVQSPSVATTASPATKEQIK--AGE 118

Qy 120 EKKAKEKIEKKGEKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYYEEV 179  
 Db 119 EKKVKETKKEKKE-KQKSAASTDSKPIDASRLDLRIGCIITAKKHPDADSLYYEEV 177  
 Qy 180 DVGEIAPRTVVGSLVNHVPLEQONRMVILLCNLKPAKMRGVLQAMVMCASSPEKIEIL 239  
 Db 178 DVGEAAPRTVVGSLVNHVPLEQONRMVILLCNLKPAKMRGVLQAMVMCASSPEKIEIL 237  
 Qy 240 APPNGSVPGDRITFDAPFGPEPKELNPKKIKWEIQPDLHTNDECVAITYKGVPEVKKG 299  
 Db 238 APPNGSVPGDRITFDAPFGPEPKELNPKKIKWEIQPDLHTNDECVAITYKGVPEVKKG 297  
 Qy 300 VCRAQTMNSGK 312  
 Db 298 VCRAQTMNSGK 310

RESULT 9  
 US-09-851-026-35  
 ; Sequence 35, Application US/09851026  
 ; Patent No. 6734168  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stern, David M.  
 ; APPLICANT: Clauss, Matthias  
 ; APPLICANT: Kao, Janet  
 ; APPLICANT: Kayton, Mark  
 ; APPLICANT: Libutti, Steven K  
 ; TITLE OF INVENTION: Endothelial Monocyte Activating  
 ; TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham, LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.30, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/851,026  
 ; FILING DATE: 07-May-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/360,821  
 ; FILING DATE: 08-OCT-96  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-278-0400  
 ; TELEFAX: 212-391-0525  
 ; INFORMATION FOR SEQ ID NO: 35:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 310 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
 ; US-09-851-026-35

Query Match 85.4%; Score 1343; DB 4; Length 310;  
 Best Local Similarity 85.9%; Pred. No. 1.5e-115;  
 Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;  
 Qy 1 MANNDVLRLEQKGAEDQIIEYLKQVSLKKEKAILQATLREBKLRVENAKLKKEIE 60  
 Db 1 MATNDVLRLEQKGAEDQIIEYLKQVSLKKEKAILQATLREBKLRVENAKLKKEIE 60





Db 121 KKKIWEIQPDLHTNAECVATYKGAPFEVKGVCRAQTWANSIGK 166

RESULT 12

US-08-360-821B-11  
; Sequence 11, Application US/08360821B  
; Patent No. 6228837  
; GENERAL INFORMATION:

APPLICANT: Stern, David M.  
APPLICANT: Clauss, Matthias  
APPLICANT: Kao, Janet  
APPLICANT: Kayton, Mark  
APPLICANT: Libutti, Steven K

TITLE OF INVENTION: Endothelial Monocyte Activating  
Polypeptide II: A Mediator Which Activates Host Response

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham, LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.30, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,821B  
FILING DATE: 08-OCT-96

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-08-360-821B-11

Query Match 53.1%; Score 835; DB 3; Length 166;  
Best Local Similarity 94.0%; Pred. No. 3.9e-69;  
Matches 156; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 147 SKPIDVSRDLRIGCIITARKHPDADSLYVEVDVGEIAPRTVSGLVNHPLEQMQRN 206

Db 1 SKPIDASRLDLRIGCIIVTAKKHPDADSLYVEVDVGEAAPRTVSGLVNHPLEQMQRN 60

Qy 207 VLLCNLKPAMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAPFGEPPDKELNP 266

Db 61 VVLLCNLKPAMRGVLSQAMVMCASSPKVKVIELAPPNGSVPGDRITFDAPFGEPPDKELNP 120

Qy 267 KKKIWEIQPDLHTNDECVAATYKGVPPFVKGVCGVCAQTMSNSGK 312

Db 121 KKKIWEIQPDLHTNAECVATYKGAPFEVKGVCRAQTWANSIGK 166

RESULT 13

US-09-851-026-11

; Sequence 11, Application US/09851026  
; Patent No. 6734168  
; GENERAL INFORMATION:

APPLICANT: Stern, David M.

APPLICANT: Clauss, Matthias

APPLICANT: Kao, Janet

; Kayton, Mark  
; Libutti, Steven K

TITLE OF INVENTION: Endothelial Monocyte Activating  
Polypeptide II: A Mediator Which Activates Host Response

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham, LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.30, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/851,026  
FILING DATE: 07-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/360,821  
FILING DATE: 08-OCT-96

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-851-026-11

Query Match 53.1%; Score 835; DB 4; Length 166;  
Best Local Similarity 94.0%; Pred. No. 3.9e-69;  
Matches 156; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 147 SKPIDVSRDLRIGCIITARKHPDADSLYVEVDVGEIAPRTVSGLVNHPLEQMQRN 206

Db 1 SKPIDASRLDLRIGCIIVTAKKHPDADSLYVEVDVGEAAPRTVSGLVNHPLEQMQRN 60

Qy 207 VLLCNLKPAMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAPFGEPPDKELNP 266

Db 61 VVLLCNLKPAMRGVLSQAMVMCASSPKVKVIELAPPNGSVPGDRITFDAPFGEPPDKELNP 120

Qy 267 KKKIWEIQPDLHTNDECVAATYKGVPPFVKGVCGVCAQTMSNSGK 312

Db 121 KKKIWEIQPDLHTNAECVATYKGAPFEVKGVCRAQTWANSIGK 166

RESULT 14

US-09-392-772-10

; Sequence 10, Application US/09392772  
; Patent No. 6346403  
; GENERAL INFORMATION:

APPLICANT: Famodu, Layo O.

APPLICANT: Antoni Rafalski

TITLE OF INVENTION: Methionine Metabolic Enzymes

FILE REFERENCE: BB-1241

CURRENT APPLICATION NUMBER: US/09/392,772

CURRENT FILING DATE: 1999-09-07

EARLIER APPLICATION NUMBER: 60/099,519

EARLIER FILING DATE: 1998-09-08

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Microsoft Office 97



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 21:51:44 ; Search time 159 Seconds  
(without alignments)  
764.514 Million cell updates/sec

Title: US-10-623-567A-1

Perfect score: 1573

Sequence: 1 MANNDVAVLKRLKQGAADQ.....FEVKGKGVCRQATMSNSGIK 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US10F\_PUBCOMB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1573	100.0	312	17	US-10-494-940-47
2	1573	100.0	312	17	US-10-623-567A-1
3	1568	99.7	312	9	US-09-851-026-36
4	1343	85.4	310	9	US-09-851-026-35
5	951	60.5	183	17	US-10-910-403-7
6	835	53.1	166	9	US-09-851-026-11
7	831	52.8	166	10	US-09-930-169-3
8	831	52.8	166	16	US-10-823-730-3
9	709	45.1	147	10	US-09-930-169-1
10	709	45.1	147	16	US-10-823-730-1
11	528	33.6	353	15	US-10-424-599-180396

12	517.5	32.9	377	16	US-10-425-115-350232	Sequence 350232,
13	517	32.9	804	16	US-10-437-963-183001	Sequence 183001,
14	516	32.8	108	10	US-09-930-169-2	Sequence 2, Appli
15	516	32.8	108	16	US-10-823-730-2	Sequence 2, Appli
16	511	32.5	792	16	US-10-437-963-183003	Sequence 183003,
17	510.5	32.5	810	15	US-10-425-114-37579	Sequence 37579, A
18	506.5	32.2	802	16	US-10-425-115-350231	Sequence 350231,
19	497.5	31.6	192	16	US-10-767-701-36700	Sequence 36700, A
20	451	28.7	536	9	US-09-813-718-2	Sequence 2, Appli
21	451	28.7	536	15	US-10-240-527A-2	Sequence 2, Appli
22	451	28.7	536	16	US-10-240-527A-2	Sequence 2, Appli
23	450	28.6	528	16	US-10-370-715B-372	Sequence 372, App
24	440.5	28.0	301	10	US-09-919-039-132	Sequence 132, App
25	430.5	27.4	178	9	US-09-813-718-6	Sequence 6, Appli
26	430.5	27.4	178	15	US-10-240-532-6	Sequence 6, Appli
27	430.5	27.4	178	16	US-10-240-527A-6	Sequence 2, Appli
28	429.5	27.3	168	17	US-10-910-403-2	Sequence 157861,
29	412	26.2	299	15	US-10-424-599-157861	Sequence 44089, A
30	407.5	25.9	423	16	US-10-767-701-44089	Sequence 109255,
31	402	25.6	409	16	US-10-437-963-109255	Sequence 197042,
32	389.5	24.8	351	16	US-10-425-115-197042	Sequence 53595, A
33	378	24.0	267	15	US-10-425-114-53595	Sequence 327897,
34	378	24.0	267	16	US-10-425-115-327897	Sequence 361131,
35	370.5	23.6	141	16	US-10-425-115-361131	Sequence 240858,
36	369.	23.5	256	15	US-10-424-599-240858	Sequence 41506, A
37	366	23.3	254	16	US-10-767-701-41506	Sequence 163246,
38	337.5	21.5	185	16	US-10-437-963-163246	Sequence 283649,
39	315.5	20.1	217	16	US-10-425-115-283649	Sequence 22, Appli
40	293	20.6	58	9	US-09-813-718-22	Sequence 22, Appli
41	293	18.6	58	15	US-10-240-532-22	Sequence 22, Appli
42	293	18.6	58	16	US-10-240-527A-22	Sequence 304067,
43	291.5	18.5	364	16	US-10-425-115-304067	Sequence 197045,
44	253	16.1	158	16	US-10-425-115-197045	Sequence 157860,
45	233	14.8	307	15	US-10-424-599-157860	

ALIGNMENTS

RESULT 1  
US-10-494-940-47  
; Sequence 47, Application US/10494940  
; Publication No. US20050069886A1  
; GENERAL INFORMATION:  
; APPLICANT: Origene Technologies, Inc  
; TITLE OF INVENTION: REGULATED PROSTATE CANCER GENES  
; FILE REFERENCE: OGT 9U 803 PCT  
; CURRENT APPLICATION NUMBER: US/10/494,940  
; CURRENT FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: 60/331,042  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/331,041  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/340,251  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/344,791  
; PRIOR FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 47  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-494-940-47

Query Match 100.0%; Score 1573; DB 17; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.2e-118;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MANNDVAVLKRLKQGAADQIIIEVLKQVSLIKKAILQATLREKKLRVENAKLKKKIE 60  
Db 1 MANNDVAVLKRLKQGAADQIIIEVLKQVSLIKKAILQATLREKKLRVENAKLKKKIE 60

Qy 61 ELKQELIQAIQNGVKQIAPPSTPLHANSVSENVVQSTAVTTVSSGTEQIKGGTGDE 120  
Db 61 ELKQELIQAIQNGVKQIAPPSTPLHANSVSENVVQSTAVTTVSSGTEQIKGGTGDE 120  
Qy 121 KKAKEKIEKKGEKKKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180  
Db 121 KKAKEKIEKKGEKKKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180  
Qy 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPQKRGVLSQAMVMCASSPEKIEILA 240  
Db 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPQKRGVLSQAMVMCASSPEKIEILA 240  
Qy 241 PPNQSVPGDRITTFDAFPGEPDKELNPKKTIWEQIQPDLHTNDECVATYKGVPPFVKGV 300  
Db 241 PPNQSVPGDRITTFDAFPGEPDKELNPKKTIWEQIQPDLHTNDECVATYKGVPPFVKGV 300  
Qy 301 CRAFTMSNSGIK 312  
Db 301 CRAFTMSNSGIK 312

RESULT 2  
US-10-623-567A-1  
; Sequence 1, Application US/10623567A  
; Publication No. US20050119175A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Sunghoon  
; TITLE OF INVENTION: Method for Stimulating Wound Healing  
; FILE REFERENCE: 012679-093  
; CURRENT APPLICATION NUMBER: US/10/623,567A  
; CURRENT FILING DATE: 2003-07-22  
; PRIOR APPLICATION NUMBER: KR 10-2002-42858  
; PRIOR FILING DATE: 2002-07-22  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-623-567A-1

Query Match 100.0%; Score 1573; DB 17; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.2e-118;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MANNDVLRLEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
Qy 61 ELKQELIQAIQNGVKQIAPPSTPLHANSVSENVVQSTAVTTVSSGTEQIKGGTGDE 120  
Db 61 ELKQELIQAIQNGVKQIAPPSTPLHANSVSENVVQSTAVTTVSSGTEQIKGGTGDE 120  
Qy 121 KKAKEKIEKKGEKKKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180  
Db 121 KKAKEKIEKKGEKKKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180  
Qy 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPQKRGVLSQAMVMCASSPEKIEILA 240  
Db 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPQKRGVLSQAMVMCASSPEKIEILA 240  
Qy 241 PPNQSVPGDRITTFDAFPGEPDKELNPKKTIWEQIQPDLHTNDECVATYKGVPPFVKGV 300  
Db 241 PPNQSVPGDRITTFDAFPGEPDKELNPKKTIWEQIQPDLHTNDECVATYKGVPPFVKGV 300  
Qy 301 CRAFTMSNSGIK 312  
Db 301 CRAFTMSNSGIK 312

RESULT 3  
US-09-851-026-36  
; Sequence 36, Application US/09851026

; Patent No. US20020160957A1  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; Clauss, Matthias  
; Kao, Janet  
; Kayton, Mark  
; Libutti, Steven K  
; TITLE OF INVENTION: Endothelial Monocyte Activating Polypeptide II: A Mediator Which Activates Host Response  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham, LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.30, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/851,026  
; FILING DATE: 07-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,821  
; FILING DATE: 08-OCT-96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 312 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-851-026-36

Query Match 99.7%; Score 1568; DB 9; Length 312;  
Best Local Similarity 99.7%; Pred. No. 3e-118;  
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANNDVLRLEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
Db 1 MANNDVLRLEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
Qy 61 ELKQELIQAIQNGVKQIAPPSTPLHANSVSENVVQSTAVTTVSSGTEQIKGGTGDE 120  
Db 61 ELKQELIQAIQNGVKQIAPPSTPLHANSVSENVVQSTAVTTVSSGTEQIKGGTGDE 120  
Qy 121 KKAKEKIEKKGEKKKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180  
Db 121 KKAKEKIEKKGEKKKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180  
Qy 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPQKRGVLSQAMVMCASSPEKIEILA 240  
Db 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPQKRGVLSQAMVMCASSPEKIEILA 240  
Qy 241 PPNQSVPGDRITTFDAFPGEPDKELNPKKTIWEQIQPDLHTNDECVATYKGVPPFVKGV 300  
Db 241 PPNQSVPGDRITTFDAFPGEPDKELNPKKTIWEQIQPDLHTNDECVATYKGVPPFVKGV 300  
Qy 301 CRAFTMSNSGIK 312  
Db 301 CRAFTMSNSGIK 312

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RESULT 4
US-09-851-026-35
; Sequence 35, Application US/09851026
; Patent No. US20020160957A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; Clauss, Matthias
; Kao, Janet
; Kayton, Mark
; Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
; Polypeptide II: A Mediator Which Activates Host Response
;
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,026
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821
; FILING DATE: 08-OCT-96
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-851-026-35

Query Match 85.4%; Score 1343; DB 9; Length 310;
Best Local Similarity 85.9%; Pred. No. 4.5e-100;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

Qy 1 MANNDAVLKLEQKGAEADQIIEYLKQOYSLKKEKALQATLREKKLRVENAKLKKEIE 60
Db 1 MATNDADVLLKLEQKGAEADQIIEYLKQOYALLKKEKALQATLREKKLRVENAKLKKEIE 60

Qy 61 ELKQELIQAFIONGVKQIAPPSPGTPPLHANSWMSVENVIOSTAV-TTVSGSTKEQIKGGTGD 119
Db 61 ELKQELILAIHNGVEQVRVRLSTPLOTNCTASESVVQSPSVATTASPATKEQIK--AGE 118

Qy 120 EKAKEKIEKKGEKKEKQOSIAGSADSPIDVSRDLIRIGCIITARKHPDADSLYVEEV 179
Db 119 EKVKTEKTEKKGEKGE-KQOSAAASTDSKPIDASRLDLRIGCIIVTAKKHPDADSLYVEEV 177

Qy 180 DVGEGAPRTVVGVLNVHVPLEQMNRMVILLCNLKPAKMRGVLSSQMWVCASSPEKIEIL 239
Db 178 DVGEGAPRTVVGVLNVHVPLEQMNRMVLLCNLKPAKMRGVLSSQMWVCASSPEKVEIL 237

Qy 240 APNPGSVPGDRITFDAPPGEKPKELNPKKKIWEQIQFDLHTNDECVATYKGVPFVKGGK 299

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Db      238  APNGSVPGDRITFDAPGPGDKELNPKKKIWEQIQPDLHTNAECVATYKGAPEFVKGKG 299
Qy      300  VCRAQTMNSGIK 312
         |||||:|||||
Db      298  VCRAQTMNSGIK 310

RESULT 5
US-10-910-403-7
; Sequence 7, Application US/10910403
; Publication No. US20050048616A1
; GENERAL INFORMATION:
; APPLICANT: Coleman et al.
; TITLE OF INVENTION: Endothelial Monocyte Activating Polypeptide III
; FILE REFERENCE: PF206D1
; CURRENT APPLICATION NUMBER: US/10/910,403
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US/08/972,301
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: US 08/483,534
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-403-7

Query Match      60.5%; Score 951; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 9.9e-69;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      130  KGEKKKKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTV 189
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Db      1   KGEKKKKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTV 60
         |||||

Qy      190  VSLGVNHVPLEQMQRNVILLCNLKPAMRGVLQAMVCMCASSPEKIEILAPPNGSVPGD 249
         |||||
Db      61  VSLGVNHVPLEQMQRNVILLCNLKPAMRGVLQAMVCMCASSPEKIEILAPPNGSVPGD 120
         |||||

Qy      250  RITFDAPGPGDKELNPKKKIWEQIQPDLHTNDECVATYKGVPEFVKGVCRAQTMNS 309
         |||||
Db      121  RITFDAPGPGDKELNPKKKIWEQIQPDLHTNDECVATYKGVPEFVKGVCRAQTMNS 180
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Qy      310  GIK 312
         |||
Db      181  GIK 183

RESULT 6
US-09-851-026-11
; Sequence 11, Application US/09851026
; Patent No. US20020160957A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
;             Clauss, Matthias
;             Kao, Janet
;             Kayton, Mark
;             Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
;                     Polypeptide II: A Mediator Which Activates Host
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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US-09-851-026-35	
Query Match	85.4%; Score 1343; DB 9; Length 310;
Best Local Similarity	85.9%; Pred. No. 4.5e-100;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;	
Qy	1 MANNDVLRLEQKGAADQIIEYLRKQVSLLLKKAIIQATLRBEKKLRVENAKLKKKEIE 60
Db	1 MATNDVLRLEQKGAADQIIEYLRKQVALLKKAIIQATMREKKLRVENAKLKKKEIE 60
Qy	61 ELKQELIQAEITQNGVKQIAPSGTPLHANSMVSNVIQSTAV--TTVSSGTKEIQKGTGD 119
Db	61 ELKQELILAEITHNGVEQVRRLSTPLQTNCTASESVQSPVATTASPATKEIQK--AGE 118
Qy	120 EKKAKEIKKEKKEKKKQOISAGSADSKPIDVSRFLDIRIGCIITARKHPDADSLYVEEV 179
Db	119 EKKYKETERKKEKKE--KQOAAAASTDSPKIDAGRLDIRIGCIITVAKKHPDADSLYBEV 177
Qy	180 DVGEIAPRTVYSGLVNHNVPLOMQRNMYILLCNLKPAKMRGVLSQLMWCMASSPKIBIL 239
Db	178 DVGEAAAPRTVYSGLVNHNVPLOMQRNMYVLLCNLKPAKMRGVLSQLMWCMASSPKVBIL 237
Qy	240 APPNGSPGDRITTFDAPPGEPDKELNPKKTIWEIQPDLHTNDECVATYKGVPPFVKGKG 299

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.30, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/851,026  
FILING DATE: 07-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,821  
FILING DATE: 08-OCT-96  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-851-026-11

Query Match 53.1%; Score 835; DB 9; Length 166;  
Best Local Similarity 94.0%; Pred. No. 2e-59;  
Matches 156; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
QY 147 SKPIDVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVVSGLVNHVPLEQMQRN 206  
DB 1 SKPIDARLRLDRLIGCIITAKKHPDADSLYYVEVDVGEAARPTVVSGLVNHVPLEQMQRN 60  
QY 207 VILLCNLKPAKMRGVLQAMVMCASSPEKIEILAPPNGSVPGDRITFDAPFGPEDKELNP 266  
DB 61 VVLLCNLKPAKMRGVLQAMVMCASSPDKVEILAPPNGSVPGDRITFDAPFGPEDKELNP 120  
QY 267 KKKIWEIQPDLHTNDECVATYKGVPEVKGKVCRAQTWNSGIK 312  
DB 121 KKKIWEIQPDLHTNAECVATYKGAPEVKGKVCRAQTWNSGIK 166

RESULT 7  
US-09-930-169-3  
Sequence 3, Application US/09930169  
Publication No. US20030004309A1  
GENERAL INFORMATION:  
APPLICANT: KIM, SUNGHOON  
APPLICANT: KO, YOUNG-GYU  
TITLE OF INVENTION: IMMUNOLOGICAL ENHANCEMENT AGENT COMPRISING N-TERMINAL PEPTIDE OF  
FILE REFERENCE: 058333/0106  
CURRENT APPLICATION NUMBER: US/09/930,169  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: KR 2001-31310  
PRIOR FILING DATE: 2001-06-05  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 166  
TYPE: PRT  
ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Mammalian  
OTHER INFORMATION: protein sequence  
US-09-930-169-3

Query Match 52.8%; Score 831; DB 10; Length 166;  
Best Local Similarity 100.0%; Pred. No. 4.3e-59;  
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 91 MVSENVISQAVTTVSSGTEKQIKGGTGDEKKAKEKKEKKQSQIAGSADSKPI 150

DB 1 MVSENVISQAVTTVSSGTEKQIKGGTGDEKKAKEKKEKKQSQIAGSADSKPI 60  
QY 151 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVVSGLVNHVPLEQMQRNVILL 210  
DB 61 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVVSGLVNHVPLEQMQRNVILL 120  
QY 211 CNLKPAKMRGVLQAMVMCASSPEKIEILAPPNGSVPGDRITFDAP 256  
DB 121 CNLKPAKMRGVLQAMVMCASSPEKIEILAPPNGSVPGDRITFDAP 166

RESULT 8  
US-10-823-730-3  
Sequence 3, Application US/10823730  
Publication No. US20040185060A1  
GENERAL INFORMATION:  
APPLICANT: IMAGENE CO., LTD.  
TITLE OF INVENTION: Immunological enhancement agent comprising N-terminal peptide of  
FILE REFERENCE: NPF1918  
CURRENT APPLICATION NUMBER: US/10/823,730  
CURRENT FILING DATE: 2004-04-14  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: KopatentIn 1.71  
SEQ ID NO 3  
LENGTH: 166  
TYPE: PRT  
ORGANISM: mammalian  
US-10-823-730-3

Query Match 52.8%; Score 831; DB 16; Length 166;  
Best Local Similarity 100.0%; Pred. No. 4.3e-59;  
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 91 MVSENVISQAVTTVSSGTEKQIKGGTGDEKKAKEKKEKKQSQIAGSADSKPI 150  
DB 1 MVSENVISQAVTTVSSGTEKQIKGGTGDEKKAKEKKEKKQSQIAGSADSKPI 60  
QY 151 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVVSGLVNHVPLEQMQRNVILL 210  
DB 61 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVVSGLVNHVPLEQMQRNVILL 120  
QY 211 CNLKPAKMRGVLQAMVMCASSPEKIEILAPPNGSVPGDRITFDAP 256  
DB 121 CNLKPAKMRGVLQAMVMCASSPEKIEILAPPNGSVPGDRITFDAP 166

RESULT 9  
US-09-930-169-1  
Sequence 1, Application US/09930169  
Publication No. US20030004309A1  
GENERAL INFORMATION:  
APPLICANT: KIM, SUNGHOON  
APPLICANT: KO, YOUNG-GYU  
TITLE OF INVENTION: IMMUNOLOGICAL ENHANCEMENT AGENT COMPRISING N-TERMINAL PEPTIDE OF  
FILE REFERENCE: 058333/0106  
CURRENT APPLICATION NUMBER: US/09/930,169  
CURRENT FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: KR 2001-31310  
PRIOR FILING DATE: 2001-06-05  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 147  
TYPE: PRT  
ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Mammalian  
OTHER INFORMATION: protein sequence  
US-09-930-169-1

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; OTHER INFORMATION: Clone ID: PAT_MRT3847_133912C.1.pgp
US-10-424-599-180396

Query Match          33.6%; Score 528; DB 15; Length 353;
Best Local Similarity 43.6%; Pred. No. 3.5e-34;
Matches 113; Conservative 41; Mismatches 79; Indels 26; Gaps 4;
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Qy	56	KKEIEELKOEILQAETIQNGVKQIAFFSGTGPLHANSVMVSENVIOSTAVTTVSSTGKTEQIKG	115
Dd	119	KPLFRELKDE-----EVEFRKKTFAGSQADRIVTAEAAEQNVASQLKTKTVSDGNKKKPG	174
		:	:
Qy	116	GTGDEKKAKEIKTEKGEKKEKKOQSITAGSADSXPIDVSRLLDRIGCIITARKHPDADSLY	175
Dd	175	KSSNEAKNK-----AAAEPDITITRLDIRVLGLIIKAQKHPDADALY	215
		:	:
Qy	176	VERVDVGETAPTRTVWSGLVNHVPLEOMQRNMTLLCNLKPAKRGVLSQAMWCASSPE-	234
Dd	216	VBEIDVGEQEOTRTVWSGLVKFIPLDEMQRNKVCVLCNLKPVTTRWGITSQAMWLAASGDH	275
		:	:
Qy	235	-KTEILLAPPNGSVPGBRITFTDAPFGPBDEKLNPKKKIWEIOQPDLHTNDECATYKGVPP	293
Dd	276	TKVELVEPSSAQOGREITFPGGVEGNPDLELNNPKKWWTFLQVLDLTNHEELVACYKNVPL	335
		:	:
Qy	294	EVRKGKGVCAQTMSNSGIK	312
Dd	336	TTSA-GVCKVSSISCGSIR	353

216	VEEIDVGBEEQTRIVTSGVLVKFI	ELDEMONR.KVCVLCNLKPVTVNRGKSGQAMVLAASDGDH	275	
Db				
235	-KTEILLAPNGSVPGDRIITFDAP	PGGPDKELNPKKTIWEQI	QPDLHTNDECVATYKGVFP	293
Qy				
276	TKVELVEPPSSAAGGRIITFGYEG	PNDELNPKKWKETLQVLDLHTNEELVACYKVVPL	335	
Db				
294	EVKGKGVCAQTMSNGIK	312		
Qy				
336	TTSA-GVCKVSSISCSGIR	353		
Db				

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; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 350232
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(377)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_82583C.1.pep
; US-10-425-115-350232

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US-10-425-115-350232

Query Match      32.9%; Score 517.5; DB 16; Length 377;
Best Local Similarity 38.2%; Pred. No. 2.7e-33;
Matches 122; Conservative 50; Mismatches 84; Indels 63; Gaps 11;

Qy 18 ADQIIIEVLKQOVSLLKEKAILQATLREEKKLRVENAKLKE-----IEE 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 98 SDEVL-----RQLNLSPEENT---SLSEKG--EIAKAKSPWDFVPHGRIGKPAFLPK 147
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 62 LKQELIQAEIQNGVKIAPFSGTPLHANSVMSENVIOSTAVTTVSSGTK--EQIKGKTGD 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 148 LKDE-----DVALHREKTAGSQAERSSKAAADAANKVANQLKG--- 186

Qy 120 EKKAKEIKIEKKGEKKKQOOSIAGSADSKPID-----VSRDLRTGCIITARKHPDADSLY 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 -----TKLSDRGTGKPEPKQS--GGSKSKTADADITVAKLDIRVGLIRKAEKHDPADSLY 239

Qy 176 VEEVDVGEIAPRTTVSGLVNHVPLEQONRWILLCNLKPAKRGVLSQAMVWCASSPE- 234
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 240 VEEIDVGDTPTVVSLGVKFIPLLEEMONRKVCVLCNLKPKVAMRGKSHAMVLAASNEHD 299  
Qy 235 -KIEILAPPNGSVCDRITFDAPFGEPPDKELNPKKIWEQIQDPLHTNDECVATYKGVFP 293  
Db 300 TKVELVPPESAAGVGVRTFAGYSGEPEASLSGSKTWEKLAELHNGELVACVYKDVFP 359  
Qy 294 EVKGGVCRAQTMSNGIK 312  
Db 360 TTSA-GICKVKTIANGAIR 377

RESULT 13  
US-10-437-963-183001  
; Sequence 183001, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 183001  
; LENGTH: 804  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_80132C.1.pap  
US-10-437-963-183001

Query Match 32.9%; Score 517; DB 16; Length 804;  
Best Local Similarity 38.1%; Pred. No. 8.4e-33;  
Matches 117; Conservative 53; Mismatches 79; Indels 58; Gaps 9;

Qy 35 KAILOATLREPKL-----RVENAKLKE-----IEELKQELIOAEIQN 73  
Db 527 EVLLQNLMTPEESLFCDDKGEIAKARPDWFSAGHKIGKPSLPFLKELDEEVES---- 582  
Qy 74 GVKQIAPPSGTPPLHANSMVSENVIQSTAVTTVSSGK--BQIKGGTGDEKAKKIEKKG 131  
Db 583 -----FRNKFAGSQAERSSKAQAADAEAKKVADKLKG-----TKLSDDG 620  
Qy 132 EKKEKKQOSTAGSADSK-----PIDVSRDLRLIGCIITARKHPDADSLYVEVDVGEIAPR 187  
Db 621 QKKEQKQS--GGSKSKNAEVDVTVAKLDIRVGLIRKAQHPDADSLYVEIDVGEAPR 678  
Qy 188 TVVSLGVNHVPLEQMNQNRVTLICNLKPAKMRGVLSQAMVWCASP8--KIEILAPPNGS 245  
Db 679 TVVSLGVKFIPLLEEMONRKVCVLCNLKPKVAMRGKSHAMVLAASNEHDTKVELVEPPESA 738  
Qy 246 VPGDRITFDAPFGEPPDKELNPKKIWEQIQDPLHTNDECVATYKGVFPFVKGKVCRAQT 305  
Db 739 AVGVRTFAGYSGEPEASLNAKSTWEKLSADLHNGELVACVYKDVFPFTTSA-GVCKVKS 797  
Qy 306 MNSNGIK 312  
Db 798 IASGEIR 804

RESULT 14  
US-09-930-169-2  
; Sequence 2, Application US/09930169  
; Publication No. US20030004309A1  
; GENERAL INFORMATION:  
; APPLICANT: KIM, SUNGHOON

; APPLICANT: KO, YOUNG-GYU  
; TITLE OF INVENTION: IMMUNOLOGICAL ENHANCEMENT AGENT COMPRISING N-TERMINAL PEPTIDE OF  
; FILE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT  
; FILE REFERENCE: 058333/0106  
; CURRENT APPLICATION NUMBER: US/09/930,169  
; CURRENT FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: KR 2001-31310  
; PRIOR FILING DATE: 2001-06-05  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Mammalian  
; OTHER INFORMATION: protein sequence  
US-09-930-169-2

Query Match 32.8%; Score 516; DB 10; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.5e-34;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANNDVAVLKELEQKGAEADQIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
Db 1 MANNDVAVLKELEQKGAEADQIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
Qy 61 ELKQELIOAEIQNGVKQIAPPSGTPPLHANSMVSENVIQSTAVTTVSSG 108  
Db 61 ELKQELIOAEIQNGVKQIAPPSGTPPLHANSMVSENVIQSTAVTTVSSG 108

RESULT 15  
US-10-823-730-2  
; Sequence 2, Application US/10823730  
; Publication No. US20040185060A1  
; GENERAL INFORMATION:  
; APPLICANT: IMAGENE CO., LTD.  
; TITLE OF INVENTION: Immunological enhancement agent comprising N-terminal peptide of  
; FILE OF INVENTION: p43 as an effective component  
; FILE REFERENCE: NPF1918  
; CURRENT APPLICATION NUMBER: US/10/823,730  
; CURRENT FILING DATE: 2004-04-14  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 2  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: mammalian  
US-10-823-730-2

Query Match 32.8%; Score 516; DB 16; Length 108;  
Best Local Similarity 100.0%; Pred. No. 6.5e-34;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANNDVAVLKELEQKGAEADQIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
Db 1 MANNDVAVLKELEQKGAEADQIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60  
Qy 61 ELKQELIOAEIQNGVKQIAPPSGTPPLHANSMVSENVIQSTAVTTVSSG 108  
Db 61 ELKQELIOAEIQNGVKQIAPPSGTPPLHANSMVSENVIQSTAVTTVSSG 108

Search completed: August 3, 2005, 22:01:39  
Job time : 161 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 21:45:34 ; Search time 174 Seconds  
(without alignments)

918.211 Million cell updates/sec

Title: US-10-623-567A-1

Perfect score: 1573

Sequence: 1 MANNDVILKRLKQGAEDQ.....FEVKGKVCRAQTMSNSGIK 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1573	100.0	312	1	MCAL_HUMAN
2	1362.5	86.6	359	1	MCAL_CRIGR
3	1343	85.4	310	1	MCAL_MOUSE
4	1338	85.1	319	2	Q8C2U7
5	1084	68.9	297	2	Q7ZMY7
6	671	42.7	323	2	Q9V504
7	625.5	39.8	351	2	Q7Q8S7
8	564	35.9	917	1	SYM_CABEL
9	517	32.9	804	1	SYM_ORISA
10	499.5	31.8	149	2	O62542
11	499	31.7	797	1	SYM_ARATH
12	453.5	28.8	529	2	O6TGS6
13	451.5	28.7	529	2	O6DFZ7
14	450	28.6	527	1	SYIC_BOVIN
15	450	28.6	527	1	SYIC_HUMAN
16	446.5	28.4	527	1	SYIC_MOUSE
17	441.5	28.1	373	2	O6BY38
18	441.5	28.1	450	2	O9P6K7
19	440	28.0	528	2	Q7ZX51
20	439	27.9	528	2	Q6DIJ1
21	429	27.3	376	1	G4P1_YEAST
22	426	27.1	376	2	O6FNNO
23	423.5	26.9	371	2	Q754V3
24	415	26.4	372	2	O6CKI6
25	402	25.6	409	2	QRUPB8
26	401.5	25.5	394	2	Q6C763
27	400.5	25.5	389	2	Q93VB0
28	400.5	25.5	440	2	Q7XJM9
29	395	25.1	525	2	Q9VV60
30	391	24.9	252	2	Q7XVQ8
31	388	24.7	78	2	Q9EPV3

32	378.5	24.1	419	2	Q7SAC3
33	343	21.8	273	2	Q9MIX8
34	337.5	21.5	441	2	O97487
35	318.5	20.2	542	2	Q7QD89
36	292.5	18.6	402	2	Q8IL48
37	264	16.8	403	2	Q7RKA7
38	231.5	14.7	724	1	SYM_PYRFU
39	227	14.4	197	2	O6BTQ8
40	223.5	14.2	722	1	SYM_PYRAB
41	215	13.7	723	1	SYM_PYRHO
42	212	13.5	663	2	Q72AE2
43	209.5	13.3	685	2	Q6FE36
44	209	13.3	793	2	Q73NT9
45	207.5	13.2	618	2	Q72J48

ALIGNMENTS

RESULT 1

MCAL\_HUMAN STANDARD; PRT; 312 AA.

AC Q12904; Q96CQ9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Multisynthetase complex auxiliary component p43 [Contains:

DE Endothelial-monocyte activating polypeptide II (EMAP-II) (Small

DE Inducible cytokine subfamily E member 1)]

GN Name=SCYB1; Synonyms=EMAP2;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=95014290; PubMed=7929199;

RA Kao J., Houck K., Fan Y., Haehnel I., Libutti S.K., Kayton M.L.,

RA Grikscheit T., Chabot J., Nowygrad R., Greenberg S., Kuang W.J.,

RA Leung D.W., Hayward J.R., Kiesel W., Heath M., Brett J., Stern D.M.;

RT "Characterization of a novel tumor-derived cytokine. Endothelial-

RT monocyte activating polypeptide II,"

RL J. Biol. Chem. 269:25106-25119(1994).

RN [2]

RP SEQUENCE FROM N.A.

RP TISSUE=Pancreas;

RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Butlerfield Y.S., Krywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.F.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- SIMILARITY: Contains 1 tRNA-binding domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way



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FT DOMAIN 198 299 polypeptide II.
SQ SEQUENCE 359 AA; 39601 MW; 4D868D1B65D72C23 CRC64;

Query Match 86.6%; Score 1362.5; DB 1; Length 359;
Best Local Similarity 86.0%; Pred. No. 6.4e-71;
Matches 270; Conservative 19; Mismatches 22; Indels 3; Gaps 2;

QY 1 MANNDVAVLRLKLEQKGAADQIIIEYLKQVSLLEKKAIIQATLREKKLRVENAKLKEIE 60
DB 47 MATNDVAVLRLKLEQKGAADQIIIEYLKQVALLKKAIVLQATLREKKLRVENAKLKEIE 106
QY 61 ELKQELIQAEIQNGVKQIAPP--SGTFLHNSMVSENVIQSTAVTTVSSGTEQIKGGTG 118
DB 107 ELKQELIQAEIQNGVKQIPVQSDTPVQASSAVSTSVIQSTSVSTISCSIKHSGKG-G 165
QY 119 DEKAKKIEKKGKKEKQKQSIAGSADSKPIDVSRDLRLGICITARKHPDADSLYVEE 178
DB 166 EEKVKKEKTKGKKEKQKQSAAPSADSKPDVDSRLDLRIGRTVTVKGGHPDADSLYVEE 225
QY 179 VDVGESAPRTVSGLVNHPLEQONRWVLLCNLKPQKMGVLSQAMVMCASSPEKIEI 238
DB 226 VDVGESAPRTVSGLVNHPLEQONRWVLLCNLKPQKMGVLSQAMVMCASSPEKVEI 285
QY 239 LAPNGSVPGDRITFDAPGPEPDKELNPKKIKWIEQIQPDLTNDCEVATYKGVPEVKGK 298
DB 286 LAPNGSVPGDRITFDAPGPEPDKELNPKKIKWIEQIQPDLTNAECVATYKGVPEVKGK 345
QY 299 GVCRAQTMNSGIIK 312
DB 346 GVCRAQTMNSGIK 359

RESULT 3
MCAL MOUSE
ID MCAL MOUSE STANDARD; PRT; 310 AA.
AC P31230; Q60659;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Multisynthetase complex auxiliary component p43 [Contains:
DE Endothelial-monocyte activating polypeptide II (EMAP-II) (Small
DE inducible cytokine subfamily E member 1)].
GN Name=Scyel; Synonyms=Emap2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95014290; PubMed=7929199;
RA Kao J., Houck K., Fan Y., Haehnel I., Libutti S.K., Kayton M.L.,
RA Grikscheit T., Chabot J., Nowygrod R., Greenberg S., Kuang W.J.,
RA Leung D.W., Hayward J.R., Kistiel W., Heath M., Brett J., Stern D.M.;
RT "Characterization of a novel tumor-derived cytokine. Endothelial-
RT monocyte activating polypeptide II."
RL J. Biol. Chem. 269:25106-25119(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner B.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 145-164 FROM N.A.
RX MEDLINE=93015897; PubMed=1400342;
RA Kao J., Ryan J., Brett G., Chen J., Shen H., Fan Y.-G., Godman G.,
RA Fanilietti P.C., Wang F., Pan Y.-C.E., Stern D., Clausen M.;
RT "Endothelial monocyte-activating polypeptide II: A novel tumor-derived
RT polypeptide that activates host-response mechanisms."
RL J. Biol. Chem. 267:20239-20247(1992).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=94193665; PubMed=7545917;
RA Kao J., Fan Y., Haehnel I., Brett J., Greenberg S., Clausen M.,
RA Kayton M., Houck K., Kistiel W., Seljelid R., Burnier J., Stern D.;
RT "A peptide derived from the amino terminus of endothelial-monocyte-
RT activating polypeptide II modulates mononuclear and polymorphonuclear
RT leukocyte functions, defines an apparently novel cellular interaction
RT site, and induces an acute inflammatory response."
RL J. Biol. Chem. 269:9774-9782(1994).
CC -!- FUNCTION: Alters endothelial and monocyte functions, induces the
CC migration of monocytes and granulocytes, and induces an
CC inflammatory response in the mouse footpad model. EMAP II elicits
CC a phlogogenic response and, potentially, augments the effects of
CC the other tumor-derived cytokines.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; U01018; AAA62203.1; -.
CC EMBL; BC002054; AAH02054.1; -.
CC PIR; A55053; A55053.
CC HSSP; Q12904; 1EUJ.
CC MGP; MGI:102774; Scyel.
CC InterPro; IPR008232; EMAPII.
CC InterPro; IPR008994; Nucleic_acid_OB.
CC InterPro; IPR002547; tRNA_bind.
CC Pfam; PF01588; tRNA_bind; 1.
CC PIRSF; PIRSF005381; EMAPII; 1.
CC PROSITE; PS50886; TRBD; 1.
CC Cycokine; Protein biosynthesis; RNA-binding; tRNA-binding.
FT CHAIN 1 144 Endothelial-monocyte activating
FT PROPEP 145 310 polypeptide II.
FT DOMAIN 149 250 tRNA-binding.
FT SEQUENCE 310 AA; 33997 MW; A2F8FF52A33D03A0 CRC64;

Query Match 85.4%; Score 1343; DB 1; Length 310;
Best Local Similarity 85.9%; Pred. No. 7.3e-70;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

QY 1 MANNDVAVLRLKLEQKGAADQIIIEYLKQVSLLEKKAIIQATLREKKLRVENAKLKEIE 60
DB 47 MATNDVAVLRLKLEQKGAADQIIIEYLKQVALLKKAIVLQATLREKKLRVENAKLKEIE 60
QY 61 ELKQELIQAEIQNGVKQIAPP--SGTFLHNSMVSENVIQSTAVTTVSSGTEQIKGGTG 119
DB 107 ELKQELIQAEIQNGVKQIPVQSDTPVQASSAVSTSVIQSTSVSTISCSIKHSGKG-G 179
QY 119 DEKAKKIEKKGKKEKQKQSIAGSADSKPIDVSRDLRLGICITARKHPDADSLYVEE 179
DB 166 EEKVKKEKTKGKKEKQKQSAAPSADSKPDVDSRLDLRIGRTVTVKGGHPDADSLYVEE 225
QY 179 VDVGESAPRTVSGLVNHPLEQONRWVLLCNLKPQKMGVLSQAMVMCASSPEKIEI 238
DB 226 VDVGESAPRTVSGLVNHPLEQONRWVLLCNLKPQKMGVLSQAMVMCASSPEKVEI 285
QY 239 LAPNGSVPGDRITFDAPGPEPDKELNPKKIKWIEQIQPDLTNDCEVATYKGVPEVKGK 298
DB 286 LAPNGSVPGDRITFDAPGPEPDKELNPKKIKWIEQIQPDLTNAECVATYKGVPEVKGK 345
QY 299 GVCRAQTMNSGIIK 312
DB 346 GVCRAQTMNSGIK 359

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Db 119 EKKVKEKTEKKEKKE-KQSSAAASTDSKPIDASRLDLRIGCVITAKKHPDADSLYVEEV 177
Qy 180 DVGEIAPRTVSGLVNHPLEOMQNRVILLCNLKPAMRGVLSOAMVMCASSPEKIEIL 239
Db 178 DVGEIAPRTVSGLVNHPLEOMQNRVILLCNLKPAMRGVLSOAMVMCASSPEKIEIL 237
Qy 240 APPNGSVPGDRITFDAPFGPDKEKLNPKKIWEIQPDLTNDBCVATYKGVPEVKKGK 299
Db 238 APPNGSVPGDRITFDAPFGPDKEKLNPKKIWEIQPDLTNDBCVATYKGVPEVKKGK 297
Qy 300 VCRAQTMNSNGIK 312
Db 298 VCRAQTMNSNGIK 310

RESULT 4
ID Q8C2U7 PRELIMINARY; PRT; 319 AA.
AC Q8C2U7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430001B22 product:endothelial monocyte activating polypeptide 2, full insert sequence.
GN Name=Scyl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=1076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuani T., Tashiro H., Itoh M., Sano N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsuoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format

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RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Okamoto N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK087932; BAC40045.1; -.
DR HSSP; Q12904; 1EUJ.
DR MGD; MGI:102774; Scyl.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000049; F:trna binding; IEA.
DR InterPro; IPR008994; Nucleic acid_OB.
DR InterPro; IPR002547; tRNA bind.
DR Pfam; PF01588; tRNA bind; 1.
DR PROSITE; PS50886; TRBD; 1.
SQ SEQUENCE 319 AA; 35197 MW; B977E8FE742BESC6 CRC64;

Query Match 85.1%; Score 1338; DB 2; Length 319;
Best Local Similarity 85.3%; Pred. No. 1.5e-69;
Matches 267; Conservative 15; Mismatches 27; Indels 4; Gaps 3;

Qy 1 MANDAVLRLKLEQGAADQIIEYLKQVSLKELAILQATLREKKLRVENAKLKEIE 60
Db 10 MATNDVLRLEQKGAEADQIIEYLKQVALLKELAILQATMREKKLRVENAKLKEIE 69
Qy 61 ELKQELIQAEIQNGVKQIAPPSGTPHANSMSVENIQSTAV-TTVSSSGTKEQIKGTGD 119
Db 70 ELKQELILAEIHNGVEQVRVRLSTPQTNTASESVQSPSVATTSLATKEQIK-AGE 127
Qy 120 EKKAKEIKKGEKKEKQKQSIAGSADSKPIDVSRDLRIGCVITAKKHPDADSLYVEEV 179
Db 128 EKKVKEKTEKKEKKE-KQSSAAASTDSKPIDASRLDLRIGCVITAKKHPDADSLYVEEV 186
Qy 180 DVGEIAPRTVSGLVNHPLEOMQNRVILLCNLKPAMRGVLSOAMVMCASSPEKIEIL 239
Db 187 DVGEIAPRTVSGLVNHPLEOMQNRVILLCNLKPAMRGVLSOAMVMCASSPEKIEIL 246
Qy 240 APPNGSVPGDRITFDAPFGPDKEKLNPKKIWEIQPDLTNDBCVATYKGVPEVKKGK 299
Db 247 APPNGSVPGDRITFDAPFGPDKEKLNPKKIWEIQPDLTNDBCVATYKGVPEVKKGK 306
Qy 300 VCRAQTMNSNGIK 312
Db 307 VCRAQTMNSNGIK 319

RESULT 5
Q7ZWY7
ID Q7ZWY7 PRELIMINARY; PRT; 297 AA.
AC Q7ZWY7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Scyl-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;

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RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.; of the Drosophila melanogaster euchromatin:  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomic perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
[4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
[5]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003835; AAF59019.2; -.  
DR HSSP; Q12904; 1EUJ.  
DR IntAct; Q9V504; -.  
DR FlyBase; FBgn0033351; CG8235.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0000049; F:tRNA binding; IEA.  
DR GO; GO:0000049; F:tRNA binding; IEA.  
DR InterPro; IPR008232; EMAP11.  
DR InterPro; IPR008994; Nucleic acid OB.  
DR Pfam; PF01588; tRNA\_bind; 1.  
DR PIRSF; PIRSF005381; EMAP11; 1.  
DR PROSITE; PS50886; TRBD; 1.  
SQ SEQUENCE 323 AA; 34401 MW; 65EB6E30115F4E84 CRC64;  
Query Match 42.7%; Score 671; DB 2; Length 323;  
Best Local Similarity 44.9%; Pred. No. 4.4e-31;  
Matches 141; Conservative 57; Mismatches 88; Indels 28; Gaps 5;  
Qy 6 AVLKRLQKGAADQIIEYLLKQVSLKEKAILQATLREKKLRVENAKLKEIEELKQ 65  
Db 31 ADLQAIASNNRERAEALINSTEATISGIQ---QLVERQKQELIKENALAKEVEAALQ 86  
Qy 66 LIQAEIONGVKQIAPF-----SGTPLHANSMVSENVIOSTAVTTVSSGTEKQIKGTG 118  
Db 87 LVQLELRNGKKQIIPVGARGFCTSAAPV---VMPAEGAPATAAPAA----- 131  
Qy 119 DEKKAKEKIEKKGEKKKQKQSIAGSDSKPIDVSRDLRLGICITARKHPDADSLVVEE 178  
Db 132 -PKAKEPKKEKKEKPAEAKPA-APEAPVDVGRDLRLVGKIVEGRHPDADSLYLEK 189  
Qy 179 VDVGEIAPRTVSGLVNHPLEQMNRMVILLCNLKPAMRGVLSQAMVWCASPEKIEI 238  
Db 190 IDCGEAAPRTVSGLVNHPLEQMNRMVILLCNLKPAMRGVLSQAMVWCASPEKVEV 249  
Qy 239 LAPNGSVGDRITFDAPGEPDKEINPKKKIWEQIQDPLHTNDECVATYKGVPPFVKG 298  
Db 250 LSPAPGAVPGDLVHVEGYPVDPVSNMPPKKIPETVAPDLKTNGLVACVYKGVPPGK 309  
Qy 299 GVCRAQTMNSGK 312  
Db 310 GNVVAQTLKNVVK 323  
RESULT 7  
Q7Q8S7  
ID Q7Q8S7 PRELIMINARY; PRT; 351 AA.

AC Q7Q8S7;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE AgCP11872 (Fragment).  
GN Name=agCG47516; ORFNames=ENSANGG00000014444;  
OS Anopheles gambiae str. PEST.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.  
OX NCBI\_TaxID=180454;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PEST;  
RA Anopheles Genome Sequencing Consortium;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAB01008933; EAA09959.1; -.  
DR HSSP; Q12904; 1EUJ.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0000049; F:tRNA binding; IEA.  
DR InterPro; IPR008232; EMAP11.  
DR InterPro; IPR008994; Nucleic acid OB.  
DR Pfam; PF01588; tRNA\_bind; 1.  
DR PIRSF; PIRSF005381; EMAP11; 1.  
DR PROSITE; PS50886; TRBD; 1.  
FT NON TER 1  
SQ SEQUENCE 351 AA; 38153 MW; F3F1E2D23B1E3DPE CRC64;  
Query Match 39.8%; Score 625.5; DB 2; Length 351;  
Best Local Similarity 42.7%; Pred. No. 2e-28;  
Matches 134; Conservative 53; Mismatches 94; Indels 33; Gaps 5;  
Qy 8 LKRLQKGAADQIIEYLLKQVSLKEKAILQATLREKKLRVENAKLKEIEELKQELI 67  
Db 62 LQRLSNNRAABELSLKQE-----TENETLRQVDSCLQLV 100  
Qy 68 QAEIQNGVKQIAPFSGTPLHANS-----MVSENVIOSTAVTTVSSGTEKQ-----IKGTGD 119  
Db 101 SLEVAHGKQIIPVPTDDEVRAAGSPATVKMEPVAQPPA---AKESPEKPPAKAQKQSD 157  
Qy 120 EKKAKEKIEKKGEKKKQKQSIAGSDSKPIDVSRDLRLGICITARKHPDADSLVVEE 179  
Db 158 SKPEKPKKPKKEKKEKPAEAKPAEAPVDVGRDLRLVGKIVEGRHPDADSLVVEI 217  
Qy 180 DVGE-IAPRTVSGLVNHPLEQMNRMVILLCNLKPAMRGVLSQAMVWCASPEKIEI 238  
Db 218 DCGEPNPRTVISGLVYVPIEQMNRMVVALCNLKPAMRGVLSQAMVWCASPTDPRVEI 277  
Qy 239 LAPNGSVGDRITFDAPGEPDKEINPKKKIWEQIQDPLHTNDECVATYKGVPPFVKG 298  
Db 278 LAPPADAVPGDLVHVEGYPVDPVSNMPPKKIPETVAPDLKTNGLVACVYKGVPPGK 337  
Qy 299 GVCRAQTMNSGK 312  
Db 338 GPVKAQTLKNVVK 351  
RESULT 8  
SYM\_CABEL  
ID -SYM\_CABEL STANDARD; PRT; 917 AA.  
AC Q20970;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)  
DE (MethRS).  
GN Name=mrs-1; ORFNames=F58B3.5;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.

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OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RG MEDLINE=99069613; PubMed=9851916;
RT "The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RL Science 282:2012-2018(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
CC   diphosphate + L-methionyl-tRNA(Met).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
CC   family.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; Z73427; CRA97803.1; -.
CC PIR; T22898; T22898.
CC HSSP; Q12904; 1FL0.
CC WormBase; WBGene00003415; mrs-1.
CC WormPep; F58B3.5; CE06007.
CC InterPro; IPR008224; MetRS dimerising.
CC InterPro; IPR008994; Nucleic acid OB.
CC InterPro; IPR002300; tRNA-synt_1a.
CC InterPro; IPR001412; tRNA-synt_1.
CC InterPro; IPR002304; tRNA-synt_met.
CC InterPro; IPR009080; tRNA-synt_1a_bind.
CC Pfam; PF00133; tRNA-synt_1.
CC Pfam; PF01588; tRNA_bind_1.
CC PIRSF; PIRSF001528; MetRS dimerising; 1.
CC PRINTS; PR01041; TRNASYNTHMET.
CC TIGRFAMs; TIGR00398; metG; 1.
CC PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
CC Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis;
CC RNA-binding; tRNA-binding.
CC SITE 44 54 "HIGH" region.
CC SITE 367 371 "KMSKS" region.
CC BINDING 370 370 ATP (By similarity).
CC DOMAIN 756 857 tRNA-binding.
CC SEQUENCE 917 AA; 101713 MW; 3B42AAB314FBDFO CRC64;

Query Match 35.9%; Score 564; DB 1; Length 917;
Best Local Similarity 42.3%; Pred. No. 2.1e-24;
Matches 135; Conservative 52; Mismatches 100; Indels 32; Gaps 8;

QY 1 MANNDVLLKRLKQKAEADQII-EYLKQVSLLEKAILQATLREKKLRVENAKLKEI 59
DB 624 NASTAAAFVE-LEQGAKVISQLIAQLKK---FDQAKALF--TRNQLQDLGDKNQLTTIDV 677
QY 60 EELKQELIQAEITQNGVKQIAPF--SGTPLHANSWSENVIQSTAVTTVSSGTKEQIKGGT 117
DB 678 KTLQHQLELETAAGIKQVPEVSVCTP-----TPSTPASGLITE----- 718
QY 118 GDEKAKKEIKKGGKKEKQKQSIAGSADSKP-----IDVSLDLDRIIGCIITARKHPDADS 173
DB 719 APKKEAPSTPAPSEPKAKEQKKGKGAAPVDDTIDVGRGLDMRVGRIIKEKHPDADA 778
QY 174 LYVEVDVGETAPRTVWGLNVHNPLEQONRMWTLICNLPAKMRGVLSQAWMVCASSP 233
DB 779 LYVEQIDVGESAPRTVWGLRVHVPDQNRLLVVLICNLPAKMRGVESRAMWVCASSP 838
QY 234 EKIEIETLAPNGSVPGDRITFDAPFPGEPDKELNPKKIWEQIQPDILHTNDECVATYKGVFF 293

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Db 839 DKVEIMEVPADSRKPGTPVCPPTVTHRPDEQLNPKKIKIETWETVAEDLKVSAAGFAEWKQPL 898
QY 294 EVKKGKGVCAQQTMSNGIK 312
Db 899 LIGSESKWTAPTTLRGVHVK 917

RESULT 9
ID SYM ORYSA STANDARD; PRT; 804 AA.
AC Q9ZTS1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA
DE ligase) (MetRS).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Denizciak M., Miranda M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
CC   diphosphate + L-methionyl-tRNA(Met).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
CC   family.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
CC
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CC
CC -----
CC EMBL; AF040700; AAC99620.1; -.
CC HSSP; Q12904; 1FL0.
CC Gramene; Q9ZTS1; -.
CC InterPro; IPR008224; MetRS dimerising.
CC InterPro; IPR008994; Nucleic acid OB.
CC InterPro; IPR002300; tRNA-synt_1a.
CC InterPro; IPR001412; tRNA-synt_1.
CC InterPro; IPR002304; tRNA-synt_met.
CC InterPro; IPR002547; tRNA_bind.
CC InterPro; IPR009080; tRNA-synt_1a_bind.
CC Pfam; PF00133; tRNA-synt_1.
CC Pfam; PF01588; tRNA_bind_1.
CC PIRSF; PIRSF001528; MetRS dimerising; 1.
CC PRINTS; PR01041; TRNASYNTHMET.
CC TIGRFAMs; TIGR00398; metG; 1.
CC PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
CC Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis;
CC RNA-binding; tRNA-binding.
CC DOMAIN 4 11 Poly-Pro.
CC SITE 28 38 "HIGH" region.
CC SITE 350 354 "KMSKS" region.
CC BINDING 353 353 ATP (By similarity).
CC DOMAIN 642 745 tRNA-binding.
CC SEQUENCE 804 AA; 89716 MW; A87E8ABBD419D440 CRC64;

Query Match 32.9%; Score 517; DB 1; Length 804;
Best Local Similarity 38.1%; Pred. No. 9.3e-22;
Matches 117; Conservative 53; Mismatches 79; Indels 58; Gaps 9;

QY 35 KAILQATLREKKL-----RVENAKLKE-----IIEELKQELIQAEITQ 73
DB 527 EVLLQLNMTPEESLFCDDKGEIAKAKRPFVSGAGHKIGKPSPLFKELKDEEVES----- 582

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```
QY 74 GVKQIAPSPGTPPLHANGMWSENVIQSTAVTTVSSGTK--BOIKGGTGDEKKAKEIKKKG 131
DB 583 -----PRNFKASQASRSSKAQADAEAKKVADKLKG-----TKLSDGG 620
QY 132 EKKEKKQOISAGSADSK----PIDVSRDLRLIGCIITARKHPDADSLYVEVDVGEIAPR 187
DB 621 QKKEQKQKS--GGSKSKNAEVDVTVAKLDIRVGLIRKAQHPDADSLYVEIDVGEIAPR 678
QY 188 TVVSGLVNHPLEOMQNRWILLCNLKPAXKRGVLSOAMVWCASSPZ--KIEILAPNGS 245
DB 679 TVVSGLVKFTPLEEMQNRKVCVLCNLPKPVAMRGKSHAMVLAASNEHDHTKVELVEPPESA 738
QY 246 VPGDRITFDAPPGDPDELNPKKIWEQIOPLDHTNDECVATYKGVPEVKGKGVCAQ 305
DB 739 AVGERVTFAGYSGEPEASLNKSKTWKLSADLHNSGELVACYKDVPTTSA-GVCKVKS 797
QY 306 MNSNGIK 312
DB 798 IASGEIR 804

RESULT 10
O62542 PRELIMINARY; PRT; 149 AA.
AC O62542;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endothelial-monocyte-activating polypeptide related protein.
GN Name=EMAPR1;
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=98184040; PubMed=9523439; DOI=10.1098/rspb.1998.0311;
RA Pahler S., Krasko A., Schuetz J., Mueller I.M., Mueller W.E.G.;
RT "Isolation and characterisation of the cDNA, encoding a potential
RT morphogen from the marine sponge Geodia cydonium that is conserved in
RT higher Metazones.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 265:421-425(1998).
DR EMBL; Y14947; CAA75164.1; -.
DR HSPF; Q12904; 1FEO.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000049; F:RNA binding; IEA.
DR InterPro; IPR008994; Nucleic acid OB.
DR InterPro; IPR002547; tRNA bind.
DR Pfam; PF01588; tRNA bind. 1.
DR PROSITE; PS50886; TRBD; 1.
SQ SEQUENCE 149 AA; 16499 MW; 612728899E17C7EF CRC64;

Query Match
Best Local Similarity 62.2%; Pred. No. 1.4e-21;
Matches 92; Conservative 24; Mismatches 31; Indels 1; Gaps 1;

QY 157 LRICITARKHPDADSLYVEVDVGEIAPRTVVGVLNVHPLEOMQNRWILLCNLKP 216
DB 1 MRIGRITSVERHPADTLVVEQIDVGEKPRTCVGLVTHVAIETMNRNLVVLNLPV 60
QY 217 KMRGVLSOAMVWCASSPEKTEILAPNGSVPGDRITFDAPGEPDKEINPKKIWEQIO 276
DB 61 KMRGVTSEAMVWCASSPENIEILDPPDSCVPGDRVFTGTGTPDQLNPKKRVFTVQ 120
QY 277 DLHTNDECVATYKGVPEVKGKGVCAQ 304
DB 121 DFLVNESGVATYRGIPLQWRVR--VCAAQ 147

RESULT 11
SYM_ARATH
ID_SYM_ARATH STANDARD; PRT; 797 AA.
```

```
AC Q9SVN5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA
DE ligase) (MetRS).
GN OrderedLocusNames=At4g13780; ORFNames=F18A5.170;
OS Arabidopsis thaliana (Mouse ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopses.
OX NCBI_TaxID=3702;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Dueterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenecker T., Bothe G., Rampsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Bernaisser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarssen A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzl A.,
RA Neumann S., Ariglou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacón D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegler L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latrelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Neilson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshua C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Rameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen A., Hameed W.R.;
RT "Sequencing and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:769-777(1999).
CC -I- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -I- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
CC family.
CC -I- SIMILARITY: Contains 1 tRNA-binding domain.
CC
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QY 94 ENVI-----QSTAVTTVSSGTKEQIKGKTGDEKKA-----KEKIEKKG 131  
 DB 273 EFVILRDEKGNKNTYATYLDLEKFADEVV-HPGDLKNSVEVALNKLLDPIREKENTPA 331  
 QY 132 EKK-----EKKQSIAGSA-DSKPIDV--SRLLDLRIGCIITAKRHPDADSLYVEEV 179  
 DB 332 LKLLSSAAYPPSKQKPAVKGPAKNSPEEIPSRLLDIRVGKVISVDKHPDADSLYVEKI 391  
 QY 180 DVGEIARTVVGSLVNVHPLQMONRMVILLCNLKPAMRGVLTSGQAMVMCASSP---EKI 236  
 DB 392 DVGEAPRTVVGSLVNVHPLQMONRMVILLCNLKPAMRGVLTSGQAMVMCASSP---EKI 451  
 QY 237 EILAPPNGSVGDRITFDAP--PGSPDKELNPKKIKWIEQIQDLHTNDECATYKGVPFV 295  
 DB 452 EPLDPPAGSARGERFVNGYKQGPDEELPKPKVFEKQLADFKISDEYIAQWKQTFMT 511  
 QY 296 K-GKGVCRNA 303  
 DB 512 KMGSVSCKS 520

## RESULT 15

SYIC HUMAN  
 ID SYIC HUMAN STANDARD; PRT; 527 AA.  
 AC P54577; O43276;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Tyrosyl-tRNA synthetase, cytoplasmic (EC 6.1.1.1) (Tyrosyl--tRNA  
 DE ligase) ("tyrRS").  
 GN Name=VARS;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96133898; PubMed=8552597; DOI=10.1073/pnas.93.1.166;  
 RA Ribas de Fouplana L., Frugier M., Quinn C.L., Schimmel P.;  
 RT "Evidence that two present-day components needed for the genetic code  
 RT appeared after nucleated cells separated from eubacteria."  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:166-170(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97306356; PubMed=9162081; DOI=10.1074/jbc.272.22.14420;  
 RA Kleeman T.A., Wei D., Simpson K.L., First E.A.;  
 RT "Human tyrosyl-tRNA synthetase shares amino acid sequence homology  
 RT with a putative cytokine."  
 RL J. Biol. Chem. 272:14420-14425(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.P., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [4]  
 RL SEQUENCE OF 1-15.  
 RN TISSUE=Platelet;  
 RC MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;  
 RX Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,  
 RA Thomas G.R., Vandekerckhove J.;  
 RA "Exploring proteomes and analyzing protein processing by mass  
 RT spectrometric identification of sorted N-terminal peptides";  
 RL Nat. Biotechnol. 21:566-569(2003).  
 RN [5]  
 RP SEQUENCE OF 1-15, AND ACETYLATION SITE GLY-1.  
 RC TISSUE=B-cell lymphoma;  
 RA Bienvenut W.V.;  
 RL Unpublished observations (OCT-2004).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (1.18 ANGSTROMS) OF 3-341.  
 RX PubMed=12429773; DOI=10.1073/pnas.242611799;  
 RA Yang X.L., Skene R.J., McKee D.B., Schimmel P.;  
 RT "Crystal structure of a human aminoacyl-tRNA synthetase cytoskeleton";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15369-15374(2002).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-tyrosine + tRNA(Tyr) = AMP +  
 CC diphosphate + L-tyrosyl-tRNA(Tyr).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase  
 CC family.  
 CC -1- SIMILARITY: Contains 1 tRNA-binding domain.  
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to a  
 CC frameshift in position 353.  
 CC  
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 CC  
 CC EMBL: U40714; AAB39406.1; ALT\_FRAME.  
 CC EMBL: U89436; AAB88409.1; --  
 CC EMBL: BC001933; AAH01933.1; --  
 CC EMBL: BC004151; AAH04151.1; --  
 CC EMBL: BC016689; AAH16689.1; --  
 CC PDB: 1N3L; X-ray; A=1-371.  
 CC PDB: 1NTG; X-ray; A/B/C/D=358-527.  
 CC PDB: 1Q11; X-ray; A=1-371.  
 CC Genew; HGNC:12840; YARS.  
 CC H-invDB; HIX0000381; --  
 CC MIM; 603623; --  
 CC GO; GO:0005737; C:cytoplasm; TAS.  
 CC GO; GO:0005615; C:extracellular space; TAS.  
 CC GO; GO:0005625; C:soluble fraction; TAS.  
 CC GO; GO:0005625; F:interleukin-8 receptor binding; TAS.  
 CC GO; GO:0005153; F:tyrosine-tRNA ligase activity; TAS.  
 CC GO; GO:0006915; P:apoptosis; TAS.  
 CC GO; GO:0006437; P:tyrosyl-tRNA aminoacylation; TAS.  
 CC InterPro; IPR008994; Nucleic acid OB.  
 CC InterPro; IPR002305; tRNA-synt\_1b.  
 CC InterPro; IPR004412; tRNA-synt\_1.  
 CC InterPro; IPR002547; tRNA-synt\_1b.  
 CC InterPro; IPR002307; Tyr\_tRNA-synt\_1b.  
 CC Pfam; PF00579; tRNA-synt\_1b; 1.  
 CC Pfam; PF01588; tRNA-bind; 1.  
 CC PRINTS; PR01040; TRNASYNTHYR.  
 CC TIGRFAMs; TIGR00234; tyrS; 1.  
 CC PROSITE; PS00178; AA TRNA LIGASE I; FALSE\_NEG.  
 CC PROSITE; PS50886; TRBD; 1.  
 KW 3D-structure; Acetylation; Aminoacyl-tRNA synthetase; ATP-binding;  
 KW Direct protein sequencing; Ligase; Protein biosynthesis; RNA-binding;  
 KW tRNA-binding.  
 FT INIT MET 0 0  
 FT MOD RES 1 1 N-acetylglutamine.  
 FT SITE 43 51 "HIGH" region.

Qy	230	ASSP--EKIELAPPNGSVFGDRITFDAP-PGEPPDKELNPKKIWIQIOPDLHTNDECY	288
Db	442	ASIEGINRQVEPLDPPAGSAFGEHVFKVGYEKGPDEELKPKKVFEXKLQADFKISBECI	501
Qy	286	ATYKGVPPFEVK-GKGVCR	303
Db	502	AOWKQTNFWTKLGSISCKS	520

Search completed: August 3, 2005, 21:57:20

Job time : 177 secs

FT	SITE	221	225	"KMSKS" region.
FT	DOMAIN	363	467	tRNA-binding.
FT	HELIX	6	14	
FT	TURN	15	16	
FT	STRAND	19	21	
FT	HELIX	23	30	
FT	TURN	31	32	
FT	STRAND	36	41	
FT	STRAND	48	48	
FT	HELIX	49	51	
FT	HELIX	52	63	
FT	TURN	64	65	
FT	STRAND	67	72	
FT	HELIX	74	79	
FT	TURN	80	83	
FT	HELIX	86	107	
FT	TURN	108	108	
FT	TURN	112	113	
FT	STRAND	114	118	
FT	HELIX	119	121	
FT	TURN	122	124	
FT	HELIX	126	136	
FT	TURN	137	138	
FT	HELIX	141	147	
FT	TURN	148	151	
FT	HELIX	160	175	
FT	TURN	176	177	
FT	STRAND	180	184	
FT	HELIX	185	187	
FT	HELIX	188	197	
FT	HELIX	198	201	
FT	TURN	202	202	
FT	STRAND	207	211	
FT	STRAND	232	232	
FT	TURN	233	234	
FT	HELIX	237	245	
FT	TURN	246	246	
FT	TURN	251	252	
FT	HELIX	258	265	
FT	TURN	266	267	
FT	HELIX	268	270	
FT	TURN	271	272	
FT	STRAND	274	276	
FT	HELIX	280	282	
FT	TURN	283	283	
FT	STRAND	286	288	
FT	HELIX	291	299	
FT	TURN	300	301	
FT	HELIX	305	326	
FT	TURN	327	328	
FT	HELIX	330	339	
SQ	SEQUENCE	527 AA; 59012 MW; A7E0E3B84390579B	CRC64;	

Query Match

Best Local Similarity 28.6%; Score 450; DB 1; Length 527;

Matches 117; Conservative 51; Mismatches 67; Indels 84; Gaps 13;

Qy	44	EEKKLRYENAKLKEIEELKQELIQAEIQNG-----VKQIAPPSGTPLHANSWVS	93
Db	227	EESKIDLLDRK-----EDVKKLKKAFCEPGNVNNGVLSFIKHVLP-----LKS	272
Qy	94	ENVIQSTAVTVSSGTKEQIKGGT-----GDEKKA-----	123
Db	273	EFVI-----LRDEKMGNGKITYAYVDLEKDFAAEVVHPGDLKNSVEVALNKLDD	321
Qy	124	--KEKIEKGGEK-----EKKQOSIA-GSA-DSKPIDV--SRLDLRIGCIITARKHP	169
Db	322	PIREKFTNPALKLASAAYDDPSKQKPKAKGNSEPEVIPSRLDIRVGKIITVEKHP	381
Qy	170	DADSLYVEVDVGGIAPRTVTVSGLVNHPLEQGNRMVILLCNLKPARKGVLSQAMVMC	229
Db	382	DADSLYVEKIDVGEAPRTVTVSGLVQFVPKKEELQDRLVVVLCNLKPQKMRGVESQGMLLC	441

Qy	230	ASSP---EKIEILAPPNGSVPGDRITFDAF-PGEPDKELNPKKKIWEQIQPDLHTNDECV	285
Db	442	ASIEGINRQVEPLDPPAGSAPGEHVFKGYEKQPDEELKPKKVKFEKQLQADFKESECI	501
Qy	286	ATYKGVPPFEVK-GKGVCR	303
Db	502	AQWKQTNFMTKLGSI	520

Search completed: August 3, 2005, 21:57:20  
Job time : 177 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 21:46:39 ; Search time 41 Seconds  
(without alignments)  
732.186 Million cell updates/sec

Title: US-10-623-567A-1

Perfect score: 1573

Sequence: 1 MANNDVAVLKRLEQKGAADQ.....FEVKGKGVCAQTMSNSGIK 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1546	98.3	310	B55053	endothelial monocy
2	1343	85.4	310	A55053	endothelial monocy
3	564	35.9	917	T22898	hypothetical prote
4	499	31.7	797	T05247	methionine-trna li
5	429	27.3	376	S64113	ARC1 protein - yea
6	400.5	25.5	440	C84832	probable methionyl
7	343	21.8	273	T47822	hypothetical prote
8	223.5	14.2	722	B57074	methionyl-trna syn
9	216	13.7	723	D71091	methionine-trna li
10	205	13.0	616	SYTWT	methionine-trna li
11	198.5	12.6	110	C85968	probable trna synt
12	198.5	12.6	110	D91123	probable trna synt
13	194.5	12.4	110	G55095	hypothetical 12.3
14	191	12.1	658	D59431	methionine-trna li
15	185.5	11.8	629	E72297	methionine-trna li
16	183.5	11.7	650	A64572	methionine-trna li
17	182.5	11.6	651	F64457	methionine-trna li
18	178.5	11.3	811	E71281	methionine-trna li
19	177	11.3	660	E83656	methionyl-trna syn
20	170	10.8	656	H71867	methionine-trna li
21	168.5	10.7	114	F82090	methionyl-trna syn
22	168.5	10.7	681	C75395	methionyl-trna syn
23	168	10.7	734	B70173	methionine-trna li
24	159.5	10.1	664	A11459	methionyl-trna syn
25	158	10.0	664	S66067	methionine-trna li
26	156.5	9.9	665	D95091	methionyl-trna syn
27	156.5	9.9	679	H97958	methionine-trna li
28	155.5	9.9	664	AB1097	methionyl-trna syn
29	151	9.6	644	A97268	methionyl-trna syn

## ALIGNMENTS

### RESULT 1

B55053

endothelial monocyte-activating protein II precursor - human

C:Species: Homo sapiens (man)

C>Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 09-Dec-2002

C:Accession: B55053

R:Kao, J.; Houck, K.; Fan, Y.; Haehnel, I.; Libutti, S.K.; Kayton, M.L.; Grikscheit, T.; J.; Stern, D.M.

J. Biol. Chem. 269, 25106-25119, 1994

A:Title: Characterization of a novel tumor-derived cytokine. Endothelial-monocyte activa

A:Reference number: A55053; MUID:95014290; PMID:7929199

A:Accession: B55053

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-310 <KAO>

A:Cross-references: GB:U10117

C:Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)

Query Match 98.3%; Score 1546; DB 2; Length 310;

Best Local Similarity 99.0%; Pred. No. 1.9e-87;

Matches 309; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy	1	MANNDVAVLKRLEQKGAADQIIIEYLKQVSLLEKAILQATLRREKLRVENAKLKKEIE	60
Db	1	MANNDVAVLKRLEQKGAADQIIIEYLKQVSLLEKAILQATLRREKLRVENAKLKKEIE	60
Qy	61	ELKQELIQAEIQNGVKQIAFPSPGTPHANSVSENVIOSTAVTTVSSGCKEIKGTGDE	120
Db	61	ELKQELIQAEIQNGVKQIRFPSPGTPHANSVSENVIOSTAVTTVSSGCKEIKGTGDE	118
Qy	121	KKAKEIEKKGEKKKQOISAGSADSKPIDVSRDLRLIGCIIITARKHPDADSLYVEEVD	180
Db	119	KKAKEIEKKGEKKKQOISAGSADSKPIDVSRDLRLIGCIIITARKHPDADSLYVEEVD	178
Qy	181	VGEIAPRTVTVSGLVNHPLEQQRNRMVILLCNLPAKMRGVLSQLAMVNCASPEKIEILA	240
Db	179	VGEIAPRTVTVSGLVNHPLEQQRNRMVILLCNLPAKMRGVLSQLAMVNCASPEKIEILA	238
Qy	241	PPNGSVPGDRITFDAPGEPDKELNPKKKIWEIQPDLHTNDECVCATYKGVPPFVKGVG	300
Db	239	PPNGSVPGDRITFDAPGEPDKELNPKKKIWEIQPDLHTNDECVCATYKGVPPFVKGVG	298
Qy	301	CRAQTMSNSGIK 312	
Db	299	CRAQTMSNSGIK 310	

### RESULT 2

A55053

endothelial monocyte-activating protein II precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004



C;Species: Saccharomyces cerevisiae  
C;Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 09-Jul-2004  
C;Accession: S64113; S69425; S72274  
R;Castagnoli, L.; Paoluzi, S.; Minenkova, O.  
submitted to the Protein Sequence Database, May 1996  
A;Reference number: S64112  
A;Accession: S64113  
A;Molecule type: DNA  
A;Residues: 1-376 <CAS>  
A;Cross-references: UNIPROT:P46672; EMBL:P46672; NID:g1322627; PIDN:CAA96812.1; PID:g1322627  
A;Experimental source: strain S288C  
R;Castagnoli, L.; Paoluzi, S.; Minenkova, O.  
submitted to the EMBL Data Library, April 1996  
A;Reference number: S69417  
A;Accession: S69425  
A;Molecule type: DNA  
A;Residues: 1-376 <CAW>  
A;Cross-references: EMBL:X97644; NID:g1310710; PIDN:CAA6247.1; PID:g1310719  
R;Simos, G.; Segref, A.; Fasiolo, F.; Hellmuth, K.; Shevchenko, A.; Mann, M.; Hurt, E.C.  
EMBO J. 15, 5437-5448, 1996  
A;Title: The yeast protein Arcip binds to tRNA and functions as a cofactor for the methionyl-tRNA synthetase  
A;Reference number: S72274; MUID:97050848; PMID:8895587  
A;Accession: S72274  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-376 <STM>  
A;Cross-references: EMBL:X95481; NID:g1620459; PIDN:CAA64750.1; PID:g1620460  
C;Genetics:  
A;Gene: SGD:ARC1; G4PI  
A;Cross-references: MIPS:YGL105w; SGD:S0003073  
A;Map position: 7L  
C;Complex: homodimer  
C;Function:  
A;Description: functions as a cofactor for methionyl- and glutamyl-tRNA synthetases  
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)  
C;Keywords: cytosol; homodimer

Query Match 27.3%; Score 429; DB 2; Length 376;  
Best Local Similarity 42.7%; Pred. No. 3.7e-19;  
Matches 105; Conservative 32; Mismatches 81; Indels 28; Gaps 9;

Qy 56 KKEIE--ELKQELIQAEIQNGVQIAPPSGTPPLHANSMVSENIQSTAVTTVSSGTKEQ 112  
Db 116 KLEINHDLDPHEVIE-----KKKAPAGGAADAATAKADVDYSK-----KAKQD 160

Qy 113 IKGTGDE---KKAKEIE-KKGKK-----EKQSQIAGSADSKIDVSRDLRGICLITA 165  
Db 161 HPRGKPDDETLKGLREKAKAKAAKAAKQOQEQQKAKPEKP-KPSAIDFRVGFQKA 219

Qy 166 RKHPDADSLYVEEDVVG-EIAPRTVSGLVNHPLEOMONRMVILLCNLKPAMKRGVLSQ 224  
Db 220 IKHPDADSLYVSTIDVGDDEGRTVCSGLVGHFPDAMQERYVVVVCNLPVNRGIKST 279

Qy 225 AMVMCASPEKIEILAPPNGSVPGDRITFDAPPGE-PDKEINPKKKIWEIQPDLHTNDE 283  
Db 280 AMVLGSSNDDKVEFVEPPKSKAGDKVFFEGFGDEAPMKQLNPKKKIWEIHPHTTNDG 339

Qy 284 CVATYK 289  
Db 340 LEVIFK 345

RESULT 6  
C84832  
probable methionyl-tRNA synthetase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: C84832  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: C84832  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-440 <STO>  
A;Cross-references: UNIPROT:Q7XJMR; GB:AE002093; NID:g4895232; PIDN:AA032818.1; GSPDB:GN  
C;Genetics:  
A;Gene: At2g40660  
A;Map position: 2  
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)

Query Match 25.5%; Score 400.5; DB 2; Length 440;  
Best Local Similarity 35.6%; Pred. No. 2.5e-17;  
Matches 105; Conservative 45; Mismatches 86; Indels 59; Gaps 9;

Qy 22 IEYLKQOVSLKKAIIQATLRE-----EKKLKRVN-NAKLKKEIEELKQELQAEIQNG 74  
Db 180 VNTIQNKEELSTLFAPIPVKLPFSPFVPRPAKIVETNSNSKAAE-----G 226

Qy 75 VKQIAPPSGTPPLHANSMVSENIQSTAVTTVSSGTKEQIKGGTGDEKKAKEIKKGEKK 134  
Db 227 VKPVDKPDVQF-----QLGTTK-----TEPEPKNAAKEKDAKK 261

Qy 135 EKQSQIAGSADSKP-----IDVSRDLRGICITITARKHPDADSLYVEEDVGEIAPRT 188  
Db 262 EKKK-----PAEPEPAKKEAELSVSLNIIQVGLIRKAWKHPADSLSLVEEDVGEDKVRQ 316

Qy 189 VVSLGNVHPLEOMONRMVILLCNLKPAMKRGVLSQAMVMCASPEK--IILAPPNGSV 246  
Db 317 VVSLGAKFCSPEDLTNRLVALITVVKPKGLRDVMSQGLVLCASSEDHSVVEPLPPAGAK 376

Qy 247 PGDRITFDAPPGEFDKELNPKKKIWEIQPDLHTNDECVATYKGVPPFVKGGKVC 301  
Db 377 PGRVSVSGIEGKPEDVLPNPKKQLEKITPGLYTDENGATYKGIQF-MTSAGPC 430

RESULT 7  
T47822  
hypothetical protein F24G16.250 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 17-Feb-2003  
C;Accession: T47822  
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;  
submitted to the Protein Sequence Database, February 2000  
A;Reference number: Z24477  
A;Accession: T47822  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-273 <DAN>  
A;Cross-references: EMBL:AL138647  
A;Experimental source: cultivar Columbia; BAC clone F24G16  
C;Genetics:  
A;Map position: 3  
A;Introns: 157/3; 226/3  
A;Note: F24G16.250  
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)

Query Match 21.8%; Score 343; DB 2; Length 273;  
Best Local Similarity 37.8%; Pred. No. 4.6e-14;  
Matches 84; Conservative 40; Mismatches 56; Indels 40; Gaps 7;

Qy 101 AVTTVSSGTKEQIKGGTGDEKKAKEIKKGEKKKQSQIAGSADSKPIDVSRDLRG 160  
Db 80 AGTTVSA-----DESEKKSE-SQKEENVKETA-----NLLDIKVG 114

Qy 161 CIITARKHPDADSLYVEEDVGEIAPRTVSGLVNHPLEOMONRMVILLCNLKPAMKRG 220  
Db 115 RIVKAWQHEEADSLYVEEDVGEIAPRTVSGLVNHPLEOMONRMVILLCNLKPAMKRG 174

Qy 221 VLSQAMVMCAS--SPEKIEILAPPNGSVPGDRITFDAPPGEFDKELN-----KKK 269  
Db 175 VKSCMLLAASDAAHENVLLVPPGSGVPGDRVWFG---NEEDLEQLPEAPPNKKVQKKK 231

Query Match 14.2%; Score 223.5; DB 2; Length 722;  
 Best Local Similarity 29.7%; Pred. No. 2.8e-06;  
 Matches 77; Conservative 52; Mismatches 75; Indels 55; Gaps 13;

Qy 14 KGADADQIIIEYLKQVSLLEKKA---ILQATLREBK-----LRVENAKLKKEIEEL--- 62  
 Db 477 KTAKEDKVRGTGTTVNSISQIVKALGILPELPDASEKIWHLLNLDVKK-RWFEPLPAG 535

Qy 63 ----KQELIOAEIQNGVKQIAF-----PSGTPPHANSMV-----ENVIOSTAVTVSS 107  
 Db 536 HKVRKPEILFKKVTD--DQIIYFILNYMAKNPEGARILLDKYKREDVIRV----- 585

Qy 108 GTKEIQKGGTDE-----KKAKEIEKKEKQKQSIAGSADSKPIDVSRDLRLGCI 162  
 Db 586 -AKEKF-----GDEAEVVLRRYVDIKLK-EKKEGEMVY-----KPDFAKDLRLVGKI 633

Qy 163 ITARKHPDADSLYVEEDVGEIAPRTVVSGLVNHVPLEQMONRMVILLCNLKPAMRGVL 222  
 Db 634 IEVKDHNADKLYVVKDLGD-EVRTLVAGLKYYKPEELNRRVVVNLEPKLRGIG 692

Qy 223 SQAMVMCASPEKIEIILAP 241  
 Db 693 SQGMLLAADDGERVALLMP 711

RESULT 9  
 D71091  
 methionine-tRNA ligase (EC 6.1.1.10) - Pyrococcus horikoshii  
 C;Species: Pyrococcus horikoshii  
 C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 16-Aug-2004  
 C;Accession: D71091  
 R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushiida, N.; Oguchi  
 DNA Res. 5, 55-76, 1998  
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
 A;Reference number: A71000; MUID:98344137; PMID:9679194  
 A;Accession: D71091  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-723 <KAW>  
 A;Cross-references: UNIPROT:O58721; GB:AP000004; NID:G3236131; PIDN:BAA30090.1; PID:G325  
 A;Experimental source: strain OT3  
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 C;Genetics:  
 A;Gene: PH0993  
 C;Superfamily: methionyl-tRNA synthetase, dimer-forming  
 C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 13.7%; Score 216; DB 2; Length 723;  
 Best Local Similarity 29.1%; Pred. No. 8.1e-06;  
 Matches 71; Conservative 53; Mismatches 72; Indels 48; Gaps 11;

Qy 20 QIIEYLKQVSLLEKKAIIQATLREBKLRVENAKLKKEIEEL-----KQELIOAEIQ 72  
 Db 495 QIVKAL-----GILLEPFLPDASEKIWHLLNLDVKK-KWFKELPAGHRVRKABILFKKVT 549

Qy 73 NGVKQIAF-----PSGTPPHANSMVSENVIOSTAVTVSSGTEKQIKGGTGD-- 120  
 Db 550 D--EQIYFILNYMGRNPEGA-----KMLLEKYYKREDVIRV-----KEKF-----GEESK 595

Qy 121 ---KKAKEIEKKEKQKQSIAGSADSKPIDVSRDLRLGCIITARKHPDADSLYVE 177  
 Db 596 IILKRYIKDLKEEGKEKEMEV-----KPEDPAKDLRLVGKILIEVKDHPNADKLYIV 649

Qy 178 EVDVGEIAPRTVVSGLVNHVPLEQMONRMVILLCNLKPAMRGVLQAMVMCASPEKIE 237  
 Db 650 KVDLGK-EVRTLVAGLKYYKPEELNKKYIIVANLEPKLRGVESQGMLLAADDGENVA 708

Qy 238 ILAP 241  
 Db 709 LLMP 712

RESULT 10  
 SYTNMT  
 methionine-tRNA ligase (EC 6.1.1.10) - Thermus aquaticus  
 N;Alternate names: methionyl-tRNA synthetase  
 C;Species: Thermus aquaticus  
 C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Dec-2002  
 C;Accession: A39517  
 R;Nureki, O.; Muramatsu, T.; Suzuki, K.; Kohda, D.; Matsuzawa, H.; Ohta, T.; Miyazawa, T  
 J. Biol. Chem. 266, 3268-3277, 1991  
 A;Title: Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus thermophilus  
 esis.  
 A;Reference number: A39517; MUID:91131636; PMID:1993699  
 A;Accession: A39517  
 A;Molecule type: DNA  
 A;Residues: 1-616 <NUR>  
 A;Cross-references: GB:M64273; GB:J05744; NID:G155135; PIDN:AAA27510.1; PID:G155136  
 A;Experimental source: strain HB8, ATCC 27634  
 A;Note: the authors translated the codon TAC for residue 323 as Thr  
 C;Genetics:  
 A;Gene: metS  
 C;Superfamily: methionyl-tRNA synthetase, dimer-forming  
 C;Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; protein biosynthesis  
 F;13,19,50,300/Active site: Tyr, His, Asp, Lys #status Predicted

Query Match 13.0%; Score 205; DB 1; Length 616;  
 Best Local Similarity 28.7%; Pred. No. 3.2e-05;  
 Matches 71; Conservative 45; Mismatches 89; Indels 42; Gaps 10;

Qy 21 IIEYLKQVSLLEKKAIIQATLREBKLRVENAKLKKEIEELKQELIOAEIQNGVKQ 77  
 Db 394 LVRELKHFHVALEAMAYVVALNYINEKPEWEL----FKKEPEEARAVLYR--VVEGLR- 446

Qy 78 IAPSGTTPPHANSMVSENVIOSTAVTVSSGTEKQI-----KGGTDEKAKEKEIKKG 131  
 Db 447 IASILLTPAMPDQK-----AELRRALGLKEEVRLEAEERWGLAEPRIPEEAPVLF 497

Qy 132 EKKEKQKQSIAGSADSKP-----IDVSRDLRLGCIITARKHPDADSLYVEEDVGE 183  
 Db 498 PKKEAK-----VEAKPEEAWIGIEDFAKLSRVAEVLAAEKHPNADRLVLRLSLGN 550

Qy 184 IAPRTVVSGLVNHVPLEQMONRMVILLCNLKPAMRGVLQAMVMCASPEKIEIILAPPN 243  
 Db 551 -ESRTVVSGLAKVYRPEELVGKKVVLVANLKPALRGIESQGMILAAQEAL-ALVTVE 608

Qy 244 GSVPGDR 250  
 Db 609 GEVPPGR 615



C1Species: Escherichia coli

QY 223 SQAMVMCASSPEKIEILAPF

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|:|::| |::| |::| |::| |::|
Db      629 SRGMILAAEXDGRKAVLLTPEKEVEPGTRV 657

RESULT 15
E72297
methionine-tRNA ligase (EC 6.1.1.10) - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: E72297
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: E72297
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-629 <ARN>
A;Cross-references: UNIPROT:O33925; GB:AE001769; GB:AE000512; NID:g4981619; PIDN:AAD3616
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1085
C;Superfamily: methionyl-tRNA synthetase, dimer-forming
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match      11.8%; Score 185.5; DB 2; Length 629;
Best Local Similarity 26.2%; Pred. No. 0.0005;
Matches 50; Conservative 46; Mismatches 72; Indels 23; Gaps 4;

Qy      83  GTPLHANSMVSENVIOSTAVTTVSSGTEQIKGGTGDEKKAKEKIE----- 128
Db      441  GTVLV-NSLEAVFKVALMTLPVMPDTSSEVFRVRSPEEKPSKEHLENGWVLPKPGSTVIHG 499

Qy      129  ----KKGEKEKKQOSTAGSADSKPI---DVSRLDIRIGCIITARKHPDADSLYVEVDV 181
Db      500  EPLFKKIDAKDFKQWETVSAEQNAITDDFSKVDLRIAKVLBAEKVPNSRKLRLIIDL 559

Qy      182  GETAPRTVWSGLVNVHPLEQMNVRVILLCNLKPAMRGVLVSQAMVWCASSPEKIBILAP 241
Db      560  G-TEKRQIVAGIAEHYEPSELVGLKLIIVVANLPAKLMGIESQGMLLAKSGDTRLITV 618

Qy      242  PNGSVPGDRIT 252
Db      619  DGEITPGAKVS 629

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XX PN WO200195927-A1.  
 XX PD 20-DEC-2001.  
 XX PF 14-JUN-2000; 2000WO-KR000630.  
 XX PR 14-JUN-2000; 2000WO-KR000630.  
 XX PA (INAG-) INAGENE CO LTD.  
 XX PI Kim S, Ko Y, Kim YS, Jo YJ;  
 XX DR WPI; 2002-098017/13.  
 XX DR N-PSDB; ABA94640.  
 XX PT Novel anti-tumor and anti-angiogenic agent of p43 comprises N-terminal  
 PT domain and C-terminal domain containing eleven beta-strands forming a  
 PT structural core and three flanking alpha-helices.  
 XX PS Claim 1; Fig 1; 35pp; English.  
 XX CC The invention provides an anti-tumor and anti-angiogenic agent of p43  
 CC consisting of two domains, the N-terminal domain (146 amino acids) and C-  
 CC terminal domain (166 amino acids) containing 11 beta-strands forming a  
 CC structural core and 3 flanking alpha-helices. p43 is useful as an anti-  
 CC tumor and anti-angiogenic agent. p43 and its C-terminal cytokine domain  
 CC (EMAP II) induce regression of fibrosarcoma in immunocompromised mouse  
 CC while its N-terminal domain does not. p43 is a potent cytokine as  
 CC determined by the induction of tumor necrosis factor-alpha (TNF-alpha),  
 CC interleukin-6 (IL-6), IL-8 and matrix metalloproteinase-9 or by its  
 CC activity of chemotaxis. The present sequence represents the human p43  
 CC polypeptide  
 XX SQ Sequence 312 AA;  
 Query Match 100.0%; Score 1573; DB 5; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-135;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MANNDVLRLEQKGAADQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKKIE 60  
 Db 1 MANNDVLRLEQKGAADQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKKIE 60  
 Qy 61 ELKQELIQAEIONGVKQIAPPSGTPHANSVSENVIOSTAVTTVSSGTEQIKGGTGD 120  
 Db 61 ELKQELIQAEIONGVKQIAPPSGTPHANSVSENVIOSTAVTTVSSGTEQIKGGTGD 120  
 Qy 121 KKAKEKIEKKEKKEKQOQSTAGSADSKPIDVSRDLRLIGCIIITARKHPDADSLYVEVD 180  
 Db 121 KKAKEKIEKKEKKEKQOQSTAGSADSKPIDVSRDLRLIGCIIITARKHPDADSLYVEVD 180  
 Qy 181 VGEIAPRTVSVGLVNHVPLEQMNRMVILLCNLPAKMGVLSQAMVNCASSPEKIEILA 240  
 Db 181 VGEIAPRTVSVGLVNHVPLEQMNRMVILLCNLPAKMGVLSQAMVNCASSPEKIEILA 240  
 Qy 241 PPGSVPGDRITFDAPFGEPPKELNPKKKIWEQIQPDLHTNDECVATYKGVPPFVKGV 300  
 Db 241 PPGSVPGDRITFDAPFGEPPKELNPKKKIWEQIQPDLHTNDECVATYKGVPPFVKGV 300  
 Qy 301 CQAQTMNSNGIK 312  
 Db 301 CQAQTMNSNGIK 312  
 RESULT 2  
 ID AAO29575 standard; protein; 312 AA.  
 XX AAO29575;  
 XX AAO29575;  
 DT 27-AUG-2003 (first entry)  
 XX

DS Human Pc240 protein.  
 XX Human; differentially regulated protein; prevention; therapy; vaccine;  
 KW prostate cancer; endothelial monocyte activating polypeptide II;  
 KW Gene therapy; Pc240.  
 XX Homo sapiens.  
 XX OS  
 XX PN WO2003040331-A2.  
 XX PD 15-MAY-2003.  
 XX PF 07-NOV-2002; 2002WO-US035563.  
 XX PR 07-NOV-2001; 2001US-0331041P.  
 XX PR 07-NOV-2001; 2001US-0331042P.  
 XX PR 18-DEC-2001; 2001US-0340251P.  
 XX PR 07-JAN-2002; 2002US-0344791P.  
 XX PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
 XX PI Sun Z, Li X, Jay G, Kovacs KP, Fan W;  
 XX DR WPI; 2003-449451/42.  
 XX DR N-PSDB; AAL60070.  
 XX PT New polynucleotide for diagnosing, staging, monitoring, prognosticating,  
 PT preventing or treating, or determining the predisposition to, diseases or  
 PT conditions such as prostate cancer, and for research or forensic science.  
 XX PS Disclosure; Page 183-184; 100pp; English.  
 XX CC The present invention relates to novel differentially regulated genes and  
 CC polypeptides encoded by them. Sequences of the invention are useful in  
 CC diagnosing, staging, monitoring, prognosticating, preventing, treating or  
 CC determining the predisposition to diseases or conditions such as prostate  
 CC cancer. They may be used as molecular markers, drug targets, vaccines, in  
 CC gene therapy, research, clinical medicine or forensic science. The  
 CC present sequence is a differentially regulated prostate protein  
 CC (endothelial monocyte activating polypeptide II), Pc240  
 XX SQ Sequence 312 AA;  
 Query Match 100.0%; Score 1573; DB 6; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-135;  
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MANNDVLRLEQKGAADQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKKIE 60  
 Db 1 MANNDVLRLEQKGAADQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKKIE 60  
 Qy 61 ELKQELIQAEIONGVKQIAPPSGTPHANSVSENVIOSTAVTTVSSGTEQIKGGTGD 120  
 Db 61 ELKQELIQAEIONGVKQIAPPSGTPHANSVSENVIOSTAVTTVSSGTEQIKGGTGD 120  
 Qy 121 KKAKEKIEKKEKKEKQOQSTAGSADSKPIDVSRDLRLIGCIIITARKHPDADSLYVEVD 180  
 Db 121 KKAKEKIEKKEKKEKQOQSTAGSADSKPIDVSRDLRLIGCIIITARKHPDADSLYVEVD 180  
 Qy 181 VGEIAPRTVSVGLVNHVPLEQMNRMVILLCNLPAKMGVLSQAMVNCASSPEKIEILA 240  
 Db 181 VGEIAPRTVSVGLVNHVPLEQMNRMVILLCNLPAKMGVLSQAMVNCASSPEKIEILA 240  
 Qy 241 PPGSVPGDRITFDAPFGEPPKELNPKKKIWEQIQPDLHTNDECVATYKGVPPFVKGV 300  
 Db 241 PPGSVPGDRITFDAPFGEPPKELNPKKKIWEQIQPDLHTNDECVATYKGVPPFVKGV 300  
 Qy 301 CQAQTMNSNGIK 312  
 Db 301 CQAQTMNSNGIK 312  
 RESULT 3

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